

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 7, 2004, 08:24:20 ; Search time 160.586 Seconds
(without alignments)
3175.877 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	4900	96.5	3768	2	US-08-356-786-1
3	4900	96.5	4473	3	US-09-048-804-1
4	4900	96.5	4473	3	US-09-056-105-26
5	4900	96.5	4473	4	US-09-663-834A-3
6	4892	96.3	3768	4	US-08-811-115-2
7	4892	96.3	4530	1	US-08-229-515A-9
8	4892	96.3	4530	1	US-08-645-865-9
9	4892	96.3	4530	4	US-09-167-322-4
10	4892	96.3	4530	4	US-09-527-487-1
11	4892	96.3	4530	4	US-09-877-177A-11
12	4892	96.3	9274	4	US-09-811-115-1

Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 26, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 9, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 11, Appli
Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-625-101-1
; Sequence 1, Application US/08625101
; Patent No. 5869445
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
; TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
; TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
; TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/625,101
; FILING DATE: 01-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C7
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:

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18 3471 68.4 1872 3 US-08-422-108-2 Sequence 2, Appli
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20 1645 32.4 5532 2 US-08-475-035-3 Sequence 3, Appli
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24 1451 28.6 5555 1 US-08-484-438-3 Sequence 3, Appli
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28 1435 28.3 4905 4 US-09-170-699-3 Sequence 3, Appli
29 1435 28.3 4975 3 US-09-630-706-3 Patent No. 5183884
30 1311 25.8 4545 6 5183884-3 Sequence 1, Appli
31 1032 20.3 1958 4 US-09-570-454-1 Sequence 1, Appli
32 1032 20.3 1958 4 US-09-867-521-1 Sequence 25, Appli
33 942 18.6 1593 4 US-09-676-610B-25 Sequence 1, Appli
34 942 18.6 1868 1 US-08-658-883B-1 Sequence 26, Appli
35 942 18.6 1868 4 US-09-676-610B-26 Sequence 1, Appli
36 493 9.7 322 1 US-08-421-356-1 Sequence 1, Appli
37 493 9.7 322 4 US-09-046-783-1 Sequence 1, Appli
38 381 7.5 4149 2 US-08-737-715-1 Sequence 1137, Ap
39 381 7.5 4723 3 US-09-023-655-1137 Sequence 5, Appli
40 376 7.4 2533 3 US-09-149-922-5 Sequence 1, Appli
41 335 6.6 4989 2 US-08-625-819-1 Sequence 1, Appli
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43 333 6.6 4975 2 US-08-249-687C-1 Sequence 3, Appli
44 333 6.6 4989 2 US-08-666-392A-3 Sequence 4, Appli
45 333 6.6 4989 3 US-08-753-558-4

SEQUENCE CHARACTERISTICS:

LENGTH: 3768 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..3765
 US-08-625-101-1

Alignment Scores:

Pred. No.: 0 Length: 3768
 Score: 4900.00 Matches: 919
 Percent Similarity: 73.23% Conservativeness: 0
 Best Local Similarity: 73.23% Mismatches: 0
 Query Match: 96.49% Indels: 336
 DB: 2 Gaps: 1

US-09-493-480-6 (1-919) x US-08-625-101-1 (1-3768)

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RESULT 2

US-08-356-786-1

; Sequence 1, Application US/08356786

; Patent No. 5877305

; GENERAL INFORMATION:

; APPLICANT: Huston, James S.

; APPLICANT: Oppermann, Hermann

; APPLICANT: Houston, L. L.

; APPLICANT: Ring, David B.

; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault

; STREET: Exchange Place, 53 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3768 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3768
OTHER INFORMATION: /note= "product = "cerB-b2"
US-08-356-786-1

Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 2 Gaps: 1

US-09-493-480-6 (1-919) x US-08-356-786-1 (1-3768)

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QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
DB 781 AGTGGCATCTGTGAGCTGCACCTGCCAGCCCTGTACCTTACCAACACAGACACCTTTGAG 840
QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
DB 841 TCCTGCCCCAATCCCGAGGCGGTATACATTGGGCGCAGCTGTGTGCTGCTGCTGCTGCTG 900
QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
DB 901 TACAACTACCTTTCTACGGAGCTGGGATCTGTCACCCCTGCTGCTGCCCTGTCACACCCAA 960
QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
DB 961 GAGGTGACACAGCAGAGATGGAAACACAGCGGTGTGAGAAGTGACAGAGCCCTGTGCCCGA 1020
QY 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
DB 1021 GTGTGCTATGGTCTGGCGATGGAGCACTTGGAGAGGTGAGGGCAGTTACCACTGCCAAT 1080
QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
DB 1081 ATCCAGAGTTTCTGCTGCTGCAAGAAATCTTTTGGAGCTTGGCAATTTCTGCCGAGAGC 1140
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
DB 1141 TTTGATGGGAGACCCAGCTTCCAACTGCCCCCTCCAGCGCAGAGCTCCCAAGTGTGT 1200
QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420
DB 1201 GAGACTCTGGAAGAGATCACAGGTACCTATATACATCTCAGCATGCGCGGACAGCTGCT 1260
QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
DB 1261 GACCTCAGCGCTTCTCCAGAACCTGCAAGTAATCCGGGAGCAATTTCTGCAATATGGGCG 1320
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuArgSerLeuArgGlu 460
DB 1321 TACTCGCTGACCTGCAAGGGCTGGGCTGAGCTGGGCTGGGCTGCTGCTGCTGCTGCTG 1380
QY 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
DB 1381 CTGGGAGTGGAGCTGGCCCTCATCCACCAATACACCCACCTCTGCTGCTGTCACACGCTG 1440
QY 481 ProTyrAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
DB 1441 CCCTGGGAGCAGCTCTTTTGGGAAACCCGCAACAGCTCTGTCTCCACACTGCCAACCGGCA 1500
QY 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
DB 1501 GAGGACAGTGTGTGGCGAGGCGCTGGCTGCGCCCTGCCACCACTGTGCGGCCGAGGCACTGC 1560
QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540

Db 1561 TGGGTCAGGGCCACCCAGTGTCAACTGCAGCAGTTCCTTCGGGGCCAGAGTGC 1620
Qy ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
Db 1621 GTGGAGGAATGCCGAGTACTGCAGGGCTCCCGAGGAGTATGTGAATGCCAGGCACCTGT 1680
Qy LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 1681 TTGCCGTGCCACCCCTAGTGTGACGCCCCAGAAATGGCTCAGTGACCTGTTTGGACCGGAG 1740
Qy AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600
Db 1741 GCTGACCAAGTGTGGCTGTGCCCACTATAGGACCCCTCCCTCTGCTGGTGGCCCGCTGC 1800
Qy ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu 620
Db 1801 CCCAGCGGTGTGAACCTGACCTCTCTTACATGCCCCATCTGGAGTTTCCAGATGAGGAG 1860
Qy GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
Db 1861 GGCCCATGCCAGCTTGGCCCATCAACTGCACTGCCACCTCTGTGTGGACCTGGATGCAAG 1920
Qy GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
Db 1921 GGCTGCCCGCCGAGCAGAGAGCCAGCCCTCTGAGCTCCATCATCTCTGCCGTGGTTGGC 1980
Qy 653 ----- 653
Db 1981 ATTCTGTGTGTGGTCTTGGGGTGTCTTTGGGATCCTCATCAAGCAGCAGCAGCAG 2040
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Qy 653 ----- 653
Db 2101 ACACCTAGCGGAGCGATGCCCAACAGCGCGCAGATGCGGATCTCTGAAGAGACGGAGCTG 2160
Qy 653 ----- 653
Db 2161 AGGAAGTGAAGTGTGGATCTGGCGCTTTTGGCACAGTCTACAGGGCATCTGGATC 2220
Qy 653 ----- 653
Db 2221 CCTGATGGGGAGAAATGTGAANAATTCAGTGGCCATCAAAGTGTGAAGGGAACACATCC 2280
Qy 653 ----- 653
Db 2281 CCCAAGCCAAAGAAATCTTAGACGAGCATACGTGATGGTGTGGGTCCCA 2340
Qy 653 ----- 653
Db 2341 TATGTCTCCGCCCTTCTGGGCATCTGCTGACATCCACGGTGCAGCTGTGACACAGCTT 2400
Qy 653 ----- 653
Db 2401 ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAACCCGGAACCGCTGGGCTCCAG 2460
Qy 653 ----- 653
Db 2461 GACCTGTGAATCTGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGATGTGGGG 2520
Qy 653 ----- 653
Db 2521 CTCGTACACAGGACTTGGCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 2580
Qy 653 ----- 653
Db 2581 ATTACAGACTTGGGGTGGCTCGGCTGTGGACATTTGACGAGACAGATACCATGCAGAT 2640
Qy 653 ----- 653

Db 2641 GGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCGCGGGTTCAAC 2700
Qy 653 ----- 653
Db 2701 CACCAGAGTGTGTGTGGAGTTATGGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2760
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Db 2761 AAACCTTAGATGGATCCAGCCCGGAGATCCCTGACCTCTCTGAAAAAGGGGAGCGG 2820
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Db 2821 CTGCCCCAGCCCCCATCTGCACCAATTGATGTCTACATGATCATGTCTCAAAATTTGGATG 2880
Qy 653 ----- 653
Db 2881 ATTGACTCTGAATGTGGGCCAAGATTCGGGGAGTTGGTGTCTGAAATTCCTCCGCGATGGCC 2940
Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGGACCCCCAGCGCTTTGTGTGTCATCCAGAAATGAGGACTTGGGCCCCAGCCAGTCCCTTG 3000
Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGCACTTCTACCGCTCACTGCTGGAGGAGATGACATGGGGACCTGGTGGATGCT 3060
Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGTGTACCCAGCAGCGGCTTCTCTGTCTCCAGACCTCTGCCCGCGCTGG 3120
Qy 705 GlyMetValHisAsnHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
Db 3121 GGCAATGTCTCCACCCAGCAGCAGCGCTCATCTACAGAGTGGCGGTGGGACCTTGACA 3180
Qy 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3181 CTAGGCTGGAGCTCTGTGAAGAGGAGGCCGCCAGCTCTCCACTGGCACCTCCGAAGGG 3240
Qy 745 AlaGlySerAspValPheAspGlyAspLeuMetGlyAlaAlaLysGlyLeuGlnSer 764
Db 3241 GCTGCTCCGATGATTTGATGTGTGACCTGGGAATGGGGCAGCCAAAGGGCTGCAAGC 3300
Qy 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 3301 CTCCCCACATGATACCCCGAGCCCTCTACAGCGGTACAGTGAGGACCCACAGTACCCCTG 3360
Qy 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3361 CCTCTGAGACTGATGGCTAGCTTGGCCCCCTGACCTGCAGCCCCCAGCCTCAATATGTG 3420
Qy 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3421 AACCCAGCAGATGTTCGGCCCCCAGCCCCCTTCGCCCGAGAGGGGGCTCTGTCTGTGTC 3480
Qy 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3481 CGACTGTGTGTGCACCTCTGGAAGGCCCAAGACTCTCTCCCCAGGGAAGAAATGGGGTC 3540
Qy 845 ValLysAspValPheAlaPheGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3541 GTCAAGAGGTTTTTTGCCCTTTGGGGTGCCTGGAGAACCCCGAGTACTGTGACACCCAG 3600
Qy 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspLeu 884
Db 3601 GGAGGAGTGCCTCTCAGCCCCACCTCTCTCTGTCTTTCAGCCCCAGCTTTCACAACTTC 3660
Qy 885 TyrTyrTrpAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3661 TATTACTGGGACCAAGACCCACAGCGGGGGCTCCACCAGCACCTTCAAGGGACA 3720
Qy 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3721 CCTACGCGCAGAGAACCCAGAGTACTCTGGTCTGTGGAGCTGCCAGTGTG 3765

RESULT 3

US-09-048-804-1
 ; Sequence 1, Application US/09048804
 ; Patent No. 5968748
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett, Allan Lipton, Lois M. Witters
 ; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF
 ; TITLE OF INVENTION: HUMAN HER-2 EXPRESSION
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5968748ris LLP
 ; STREET: One Liberty Place - 46th Floor
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: U.S.A.
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 1.44 Mb diskette
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/048,804
 ; FILING DATE: Herewith
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Paul K. Legard
 ; REGISTRATION NUMBER: 38,534
 ; REFERENCE/DOCKET NUMBER: ISIS-2913
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 568-3100
 ; TELEFAX: (215) 568-3439
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4473 base pairs
 ; TYPE: Nucleic Acid
 ; STRANDEDNESS: Single
 ; TOPOLOGY: Unknown
 ; ANTI-SENSE: No
 ; US-09-048-804-1

Alignment Scores:
 Pred. No.: 0 Length: 4473
 Score: 4900.00 Matches: 919
 Percent Similarity: 73.23% Conservatives: 0
 Best Local Similarity: 73.23% Mismatches: 0
 Query Match: 96.49% Indels: 336
 DB: 2 Gaps: 1

US-09-493-480-6 (1-919) x US-09-048-804-1 (1-4473)

QY	1	MetGluLeuAlaLeuCysArgTrpGlyLeuLeuAlaLeuLeuProProGlyAla	20
DB	175	ATGGAGCTGGGGCCCTTGTGGCGCTGGGGCTCTCTCTGGCCCTCTTGGCCCCCGGAGCC	234
QY	21	AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu	40
DB	235	GGGAGCACCACCAAGTGTGCACCCGCGCAGACATGAAGCTGGCGCTCTCTGCGAGTCCCGAG	294
QY	41	ThrHisLeuAspMetLeuArgHisLeuTyTGlnGlyCysGlnValGlnGlnAsnLeu	60
DB	295	ACCCACTGGACATGCTCCGCCACCTCTACAGGGCTGCCAGGTGGTGCAGGGAAACCTG	354
QY	61	GluLeuThrTyThrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal	80
DB	355	GAACCTACCTACCTGCCACCAATGCGAGCTGTCTCTCTGCGAGGATATCCAGGAGGTG	414
QY	81	GlnGlyTyThrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100
DB	415	CAGGGCTACGTGCTCATCGCTCAACCAAGTAGGCGAGTCCCACTGCAGAGGGCTGCGG	474
QY	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyThrAlaLeuAlaValLeuAspAsnGly	120

DB	475	ATTGTGCGAGGCACCCAGCTCTTTGAGGACAACTATATGCTGCGCTGTAGCAATGGA	534
QY	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140
DB	535	GACCCGCTGAACAATACCAACCCCTGTACAGGGGCTCCCGAGGAGCCCTGCGGGAGCTG	594
QY	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln	160
DB	595	CAGCTTCGAGGCTCACAGAGATCTTGAAGGAGGGGTCTTGATCCAGCGGAACCCCCAG	654
QY	161	LeuCysTyThrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnGlnLeuAla	180
DB	655	CTCTGCTACCAAGACACGATTTGTGAAGGACATCTTCCACAAGAACCAACAGCTGGCT	714
QY	181	LeuThrLeuLeuAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
DB	715	CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTTCTCGATGTGTAG	774
QY	201	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220
DB	775	GGCTCCCGCTGTGGGAGAGATTTCTGAGGATTTGTACAGGCTGTACGCGCACTGTCTGT	834
QY	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	240
DB	835	GGCGGTGGCTGTGCCCTGCAAGGGGCCACTGCCCACTGACTGTGCCATGAGCAGTGT	894
QY	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
DB	895	GCTGCGGGCTGACGCGGCCCAAGCACTCTGACTGCTGCGCTGCTCTCACTTCAACCCAC	954
QY	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyThrAsnThrAspThrPheGlu	280
DB	955	AGTGCACTCTGTGAGCTGCACTGCCCGAGCCCTGGTCACTTACCAACACAGACAGTTGAG	1014
QY	281	SerMetProAsnProGluGlyArgTyThrPheGlyAlaSerCysValThrAlaCysPro	300
DB	1015	TCCATGCCCAATCCGAGGGCCGGTATACATTTGGCGGCCAGCTGTGTGACTGTGCTGCCC	1074
QY	301	TyrAsnTyThrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
DB	1075	TACAACCTACTTTCTACGGACGTGGGATCTGACCCCTGTGCTGCCCCCTGCACACCAA	1134
QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340
DB	1135	GAGGTGACAGCAGAGAGATGGACACAGCGGTGTGAGAGGTGACAGAGCCCTGTGCCCGA	1194
QY	341	ValCysTyThrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
DB	1195	GTGTGCTATGTGCTGGGCATGGAGCACTTGCAGAGGGTGGAGGAGTTACAGTGCACAT	1254
QY	361	IleGlnGluPheAlaGlyCysLysIlePheGlySerLeuAlaPheLeuProGluSer	380
DB	1255	ATCCAGAGTGTGCTGGCTGCAAGAGATCTTTGGAGGCTTGCAATTTCTGCCGAGAGC	1314
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400
DB	1315	TTTGATGGGAGCCACGCTCCACACTGCCCGCTCCAGCAGCAGCAGCTCCAAAGTGT	1374
QY	401	GluThrLeuGluGluIleThrGlyTyThrLeuTyThrIleSerAlaTrpProAspSerLeuPro	420
DB	1375	GAGACTCTGGAGAGATCAAGGTATACCTATATCATCTCAGCATGGCCGAGCAGCTGCT	1434
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440
DB	1435	GACCTCAGGTCTTCCAGAACCTGCAAGTAAATCCGGGAGCGAATTTCTGCACAAATGGCGC	1494
QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
DB	1495	TACTCGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGCGCTCTCATGAGGAA	1554
QY	461	LeuGlySerGlyLeuAlaIleLysHisAsnThrHisLeuCysPheValHisThrVal	480

Db 1555 CTGGGAGTGGAGCTGGCCCTCATCCACCATTAACACCCACCTCTGCTTGGTGCAACCGGTG 1614
Qy 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
Db 1615 CCTGGGACCAAGCTCTTTGGAAACCCGACCAAGCTCTGCTCCACACTGGCCAAACCGGCCA 1674
Qy 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
Db 1675 GAGGACAGGTGTGTGGCGAGGGCTGGCTGCCACCAAGCTGTGGCCCGGAGGCACTGC 1734
Qy 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Db 1735 TGGGTCACAGGCCACCCAGTGTGTCACTGACGACAGTTCCTTGGGGCCAGAGTGC 1794
Qy 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluPheValAsnAlaArgHisCys 560
Db 1795 GTGGAGGAATGCCAGTACTGCAGGGCTCCCGAGGAGTATGTGAATGCCAGGCACTGT 1854
Qy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 1855 TTGCCGTGCCACCTGAGTGTGAGCCCGACAGAAATGGCTCAGTGACCTGTGTTGGACCGGAG 1914
Qy 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
Db 1915 GCTGACAGTGTGTGGCTGTGCCACTATAGACCTCCCTTCTGCGGGCCCGCTGC 1974
Qy 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu 620
Db 1975 CCCAGCGGTGAAACCTGACCTCTCTACATGCCATCTGGAAGTTTCCAGATGAGGAG 2034
Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
Db 2035 GGGGCATGCCAGCTTGTGCCCATCACTGACCCACCTCTGTGTGGAGCTGTGATGACAAG 2094
Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
Db 2095 GGCTGCCCCCGAGCAGAGAGCCGCGCTTGACGTCATCTCTGCGGTGGTGGC 2154
Qy 653 ----- 653
Db 2155 ATTCTGCTGCTGTGGTCTTTGGGGTGTCTTTGGGATCCTCAACAGCGACGACGAG 2214
Qy 653 ----- 653
Db 2215 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGAAACGGAGCTGGTGGAGCCGCTG 2274
Qy 653 ----- 653
Db 2275 ACACCTAGCGGAGGATGCCAACCGAGCGAGATGCGGATCCTGAAAGAGACGGAGCTG 2334
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Db 2335 AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAAGGGCATCTGGATC 2394
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Db 2395 CCTGATGGGAGAAATGTGAAATTTCCAGTGGCCCATCAAGTGTGAGGGAAAAACATCC 2454
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Db 2455 CCCAAAGCCAAAGAAATCTTAGAGCAAGCATACGTGATGGCTGTGTGGGTCCCCA 2514
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Db 2515 TATGTCTCCGCTTCTGGGCATCTGCTTGACATCCACGGTGCGAGCTGTGTGACACAGCTT 2574
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Db 2575 ATGCCCTTAGGCTGCTCTTAGACCAATGTCCGGGAAAAACCGCGAGCGCTGGGCTCCAG 2634
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Db 2695 CTCTGACACAGGAGCTTGGCCGCTCGGAAACGTCGTGGTCAAGAGTCCCAACATGTCAAA 2754
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Db 2755 ATTACAGACTTTCGGGCTGGCTCGGCTGTGGACATTGACGAGACAGAGTACCATGCAGAT 2814
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Db 2815 GGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGGGTTCAAC 2874
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Qy 653 ----- 653
Db 2935 AAACCTTACGATGGGATCCCGAGCCCGGAGATCCCTGACCTGTGGAAAAGGGGAGCGG 2994
Qy 653 ----- 653
Db 2995 CTGCCCCAGCCCCCATCTGCAACCATTTGATGTCTACATGATCATGTCAAATGTTGGATG 3054
Qy 653 ----- 653
Db 3055 ATTGACTCTGAATGTCCGCCCAAGATTCCGGGAGTTGGTGTCTGAATTTCTCCGCGATGGCC 3114
Qy 654 ----- GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3115 AGGAGACCCCGAGCCCTTTGGTGCATCCAGAAATGAGGACTTGGGCCAGCCAGTCCCTTG 3174
Qy 665 AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3175 GACAGCACTTCTACCGCTCACTCTGAGGACGATGATCATATGGGGAGCTGTGTGGATGCT 3234
Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3235 GAGGAGTATCTGTGTACCCAGCAGCGGCTTCTGTCCAGACCTTGCCTCCCGCGCTGGG 3294
Qy 705 GlyMetValHisArgHisArgSerSerSerThrArgSerGlyGlyValAspLeuThr 724
Db 3295 GGCATGTCTCACCAACAGCACCGCAGCTCATCTACAGAGTGGCGGTGGGAGCTTGACA 3354
Qy 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGlyGly 744
Db 3355 CTAGGGCTGGAGCCCTCTGAAGAGAGAGGCCCCCAGGTCCTCCACTGGCACCTCCCGAAGG 3414
Qy 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
Db 3415 GCTGGCTCCGATGTATTTGATGTGTGACCTTGGGAAATGGGGGAGCCCAAGGGCTTCGAAAGC 3474
Qy 765 LeuProThrHisAspProSerProLeuGluArgTyrSerGluAspProThrValProLeu 784
Db 3475 CTCCCCACATGATGACCCCGAGCCCTCTACAGCGGTACAGTGAAGACCCCAAGTACCCCTG 3534
Qy 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3535 CCCTCTGAGACTGATGGCTAGCTTGGCCCCCTGACCTGACGCCCCCAGCCTCGAATATGTG 3594
Qy 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3595 AACCCAGCAGATGTTCGGCCCCCAGCCCCCTTTCGGCCCCGAGAGGGGCCCTCTGCTCTGCTGCC 3654
Qy 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3655 CGACCTCTGCTGCTCACTCTGGAAGGCCCAAGACTCTCTCCCAAGGAGAGATGGGGTCTC 3714
Qy 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3715 GTCAAGACGCTTTTGCCTTTGGGGTGGCGTGGAGAACCCCGAGTACTTGACACCCCGAG 3774

QY 865 GlyGlyAlaAlaProGlnProHisProProAlaAlaPheSerProAlaPheAspAsnLeu 884
Db 3775 GGAGGAGCTGCCCTCAGCCCCCACCCTCTCTCTGCTTTCAGCCAGCTTCGACAACTC 3834
QY 885 TTTTTPAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3835 TATTAATGGACAGGACCCACAGCGGGGGCTCCACCCAGCACCTTCAAGGGACA 3894

QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3895 CCTACGGCAGAGAACCCAGGATACCTGGGCTCTGGAGCTGCCAGTG 3939

RESULT 4

US-09-056-105-26

; Sequence 26, Application US/09056105

; Patent No. 6287569

; GENERAL INFORMATION:

; APPLICANT: KIPPS, THOMAS J.

; APPLICANT: KU, YUNQI

; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR

; TITLE OF INVENTION: PROCESSING

; FILE REFERENCE: 233/221

; CURRENT APPLICATION NUMBER: US/09/056,105

; CURRENT FILING DATE: 1998-04-06

; EARLIER APPLICATION NUMBER: 60/043,467

; EARLIER FILING DATE: 1997-04-10

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 26

; LENGTH: 4473

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-056-105-26

Alignment Scores:

Pred. No.:	0	Length:	4473
Score:	4900.00	Matches:	919
Percent Similarity:	73.23%	Conservative:	0
Best Local Similarity:	73.23%	Mismatches:	0
Query Match:	96.49%	Indels:	336
DB:	3	Gaps:	1

US-09-493-480-6 (1-919) x US-09-056-105-26 (1-4473)

QY 1 MetGluLeuAlaAlaLeuCysArgTyrGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
Db 175 ATGGAGCTGGCGCTTGTGCGCTGGGGCTCTCTCTGCGCTCTTGGCCCCCGGAGCC 234

QY 21 AlaSerThrGlnValCysThrGlyThrAspMetIleuArgLeuProAlaSerProGlu 40
Db 235 GCAGGACCCCAAGTGTGCACCGGCACAGACATGAAGCTGGCGCTCCCTGCGAGTCCGAG 294

QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 295 ACCCACTGGACATGCTCCGCCACCTCTACCGAGGCTGCCAGTGTGTGCGAGGAAACCTG 354

QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 355 GAACCTACCTACCTGCCCAATGCCAGCTGTCTCTCTGCGAGGATATCCAGGAGTG 414

QY 81 GluGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 415 CAGGGCTACCTGTGTATCGCTCACAACAGTGGAGGAGGTCCCACTGCGAGAGCTCCGG 474

QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 475 ATTGTGCGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGGCGCTGTAGACAAATGA 534

QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 535 GACCCGCTGAACATATACCCCTGTCTACAGGGGCTCCCGAGGAGGCTGCGGAGCTG 594

QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln 160

Db 595 CAGCTTCGAGGCTCAGAGATCTTGAAGGAGGGTCTTGTATCCAGCGAACCCTCAG 654
QY 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnGlnLeuAla 180
Db 655 CTCTCTACCAAGACACGATTTTGTGAAGGACATCTTCCACAAGAACCAACAGCTGGCT 714
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
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Qy 705 GlyMetValHisHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
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Qy 885 TyrTyrTrpAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
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QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
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Db 3895 CCTACGGCAGAGAACCCAGGTACCTGGTCTGGAGCTCCAGTG 3939

RESULT 5

US-09-663-834A-3
; Sequence 3, Application US/09663834A
; Patent No. 6613567
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowert
; TITLE OF INVENTION: ANTISENSE MODULATION OF HER-2 EXPRESSION
; FILE REFERENCE: RTS-0033
; CURRENT APPLICATION NUMBER: US/09/663,834A
; CURRENT FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 3
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (175)...(3942)
US-09-663-834A-3

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 4 Gaps: 1

US-09-493-480-6 (1-919) x US-09-663-834A-3 (1-4473)

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Db 235 GCGAGCACCCAGTGTGCACCGGCACAGACATGAAGCTGCGGCTCTCCAGTCCGAG 294
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
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Qy 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal. 919
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RESULT 6

US-09-811-115-2
; Sequence 2, Application US/09811115
; Patent No. 6632979
; GENERAL INFORMATION:

; APPLICANT: Erickson, Sharon
 ; APPLICANT: Schwall, Ralph
 ; APPLICANT: King, Kathleen
 ; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
 ; FILE REFERENCE: GENENT.034A
 ; CURRENT APPLICATION NUMBER: US/09/811.115
 ; CURRENT FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/189,844
 ; FILING DATE: 2000-03-16
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 3768
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-811-115-2

Alignment Scores:
 Pred. No.: 0 Length: 3768
 Score: 4892.00 Matches: 918
 Percent Similarity: 73.15% Conservative: 0
 Best Local Similarity: 73.15% Mismatches: 1
 Query Match: 96.34% Indels: 336
 DB: 4 Gaps: 1

US-09-493-480-6 (1-919) x US-09-811-115-2 (1-3768)

QY 1 MetGluLeuAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
 DB 1 ATGGAGCTGGCGGCTTGTGGCTGGCGGCTCTCTCGCCCTCTTGGCCCGGAGCC 60
 QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
 DB 61 GCGAGCACCAAGTGTGACCGGACAGACATGAGCTGCGGCTCTCTCGCCAGTCCCGAG 120
 QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrglnGlyCysGlnValValGlnGlyAsnLeu 60
 DB 121 ACCCACTGGAGATGCTCGGCACCTCTACCAAGGCTGCGAGTGTGTGCGGAAACCTG 180
 QY 61 GluLeuThrTyrluProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
 DB 181 GAATCACTACTCTGCCACCAATGCGAGCTGTCTCTCTGCGAGGATATCCAGGAGTG 240
 QY 81 GlnGlyTyrluValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
 DB 241 CAGGGCTACGTGCTCATCGCTCAACCAAGTGTGAGCGAGTCCCATCTGCGAGGCTGCGG 300
 QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrluAlaLeuAlaValLeuAspAsnGly 120
 DB 301 ATTGTGGAGGACACCGAGCTCTTTGAGGACACTATGCTGCGCTGCTGCTGAGACATGGA 360
 QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
 DB 361 GACCCGCTGAACAATACCACTCTGTGAGGACACTATGCTGCGCTGCTGCTGAGAGCTG 420
 QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
 DB 421 CAGCTTCGAAGCCTCAAGAGATCTTGAAGAGACATCTTCCACAGAACCAACAGCTGGCT 480
 QY 161 LeuCysTyrluGlnAspThrIleLeuTyrluAspIlePheHisLysAsnGlnLeuAla 180
 DB 481 CTCTGCTACAGGACACGATTTGTGAGAGACATCTTCCACAGAACCAACAGCTGGCT 540
 QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
 DB 541 CTCACACTGATACACCAACCGCTCTCGGGCTGCGCCCTGCGCCCTGCTTCCGATGTGTAA 600
 QY 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
 DB 601 GGCTCCCGCTGCTGGGAGAGAGTTCTGAGGATTTGTGAGAGCTGAGAGCTGAGCGCACTGCTGT 660
 QY 221 AlaGlyGlyCysAlaArgCysGlyProLeuProThrAspCysCysHisGlnGlnCys 240

DB 661 GCCGCTGGCTGTGCCCGCTGCAAGGGGCGCACTGCCCACTGACTGCTGCCATGAGCAGTGT 720
 QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
 DB 721 GCTGCCGCTGCACGGGCGCCCAAGCACTCTGACTGCTGGCTGGCTTCCACTTCAACCCAC 780
 QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrluAsnThrAspThrPheGlu 280
 DB 781 AGTGGCATCTGTGAGCTGCACTGCCCGGCGCTTGGTCACTCAACACACAGACACGTTTGA 840
 QY 281 SerMetProAsnProGluGlyArgTyrluPheGlyAlaSerCysValThrAlaCysPro 300
 DB 841 TCCATGCCCAATCCCGAGGGCGGTATACATTCGGCGCGCAGCTGTGTGACTGCTGTCCC 900
 QY 301 TyrluAsnTyrluSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
 DB 901 TACAACCTACTCTTACGGACGTGGATCTCGACCTCTGCTGCTGCTGCTGCAACACCAA 960
 QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
 DB 961 GAGGTGACAGCAGAGATGGAACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGTGCCCGA 1020
 QY 341 ValCysTyrluGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
 DB 1021 GTGTGCTATGTGCTGGGCAATGGAGCACTTGGCGAGAGTGTGAGGCGAGTTACCACTGCCAAT 1080
 QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
 DB 1081 ATCCAGGAGTGTGCTGGCTGCAAGAGATCTTTGGGAGCTGGCATTTTCCCGGAGGC 1140
 QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
 DB 1141 TTTGATGGGACCCAGCTTCCAACTGCCCCCTCCAGCCAGCAGCAGCTCCAAAGTGT 1200
 QY 401 GluThrLeuGluGluIleThrGlyTyrluTyrluIleSerAlaValProAspSerLeuPro 420
 DB 1201 GAGACTCTGGAAGAGATCACAGTTTACCTATATACATCTCAGCATGTGGCGGACAGCTGCT 1260
 QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyVala 440
 DB 1261 GACCTCAGCGCTTCCAGAACCTGCAAGTAATCCGGGAGCAATTTCTGCACATGGGCGC 1320
 QY 441 TyrluSerLeuThrLeuGlnGlyLeuGlyIleSerTyrluLeuArgSerLeuArgGlu 460
 DB 1321 TACTGCTGACCTTGCAGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 1380
 QY 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
 DB 1381 CTGGGAGTGTGAGTGGCTTCCATCCACCAATTAACCCACCTCTGCTGCTGCTGCTGCTG 1440
 QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
 DB 1441 CCTGGGAGCAGCTCTTTGGGAACCCCGACCAAGCTCTGCTCCACACTGCTCCACCCGCGCA 1500
 QY 501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
 DB 1501 GAGGACAGTGTGTGGCGGAGGCGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 1560
 QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
 DB 1561 TGGGCTCCAGGGCGCCACCCAGTGTGTCACTGAGCGAGTGTCTTCTGGGCGGAGAGTGT 1620
 QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGlyTyrluValAsnAlaArgHisCys 560
 DB 1621 GTGGAGGAATGCGAGTACTGAGGGGCTCCCGAGGAGTATGTGATGATGCCAGCAGCTGT 1680
 QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
 DB 1681 TTCCGCTGGCCACCTGAGTGTGAGCGCCACCAATGGCTCAGTGCCTGCTTTTGGACCGGAG 1740
 QY 581 AlaAspGlnCysValAlaCysAlaHisTyrluAspProPheCysValAlaArgCys 600
 DB 1741 GCTGACCGAGTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGT 1800

Qy 601 ProSerGlyValIysProAspLeuSerTyrMetProIleThrLysPheProAspGluGlu 620
Db 1801 CCCAGCGGTGTAACCTGACCTCTCCCTACATGCCCATCTGGAAAGTTTCCAGATGAGGAG 1860
Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
Db 1861 GGCGCATGCCAGCTTGGCCCCATCACTGACCCACTCTCTGTGTGGACTGTGATGACAAAG 1920
Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
Db 1921 GGCTGCCCGCGAGCAGAGAGCCAGCCCTCTGAGCTCCATCTCTCGGTGGTTGGC 1980
Qy 653 ----- 653
Db 1981 ATCTGTGTCGTGTCCTTGGGGTGTGTTTGGGATCTCTATCAAGCAGCGAGCAG 2040
Qy 653 ----- 653
Db 2041 AAGATCCGGAAAGTACACGATGGGAGACTGTCTGCAGGAACGGAGCTGGTGGAGCCGCTG 2100
Qy 653 ----- 653
Db 2101 ACACCTAGCGGAGCGATGCCCAACCGAGCGCAGATGCCGATCCTGAAGAGACGGAGCTG 2160
Qy 653 ----- 653
Db 2161 AGGAAGTGAAGTGTCTGGATCTGGCGCTTTTGGCACAGTCTACAGGGCATCTGGATC 2220
Qy 653 ----- 653
Db 2221 CCTGATGGGAGAAATGTGAAATTCAGTGGCCATCAAAGTGTGAGGGAACACATCC 2280
Qy 653 ----- 653
Db 2281 CCCAAGCCACAAAGAAATCTTAGACGAAGCATAGTGGCTGTGGCTCCCA 2340
Qy 653 ----- 653
Db 2341 TATGTCTCCCGCTTCTGGGCATCTGCTGACATCCAGGTGCAGCTGGTGACACAGCTT 2400
Qy 653 ----- 653
Db 2401 ATGCCCTATNGCTGCTCTTAGACCATGTCTCGGGAACCCGGAGCGCTGGGCTCCAG 2460
Qy 653 ----- 653
Db 2461 GACCTGCTGAACCTGTATCCAGATTGCCAAGGGGATGACTACCTGGAGGATGTGGG 2520
Qy 653 ----- 653
Db 2521 CTCGTACACAGGACTTGGCGCTCGGAACTGTGCTCAAGAGTCCCAACCATGTCAAA 2580
Qy 653 ----- 653
Db 2581 ATTACAGACTTGGGCTGGCTGGCTGTGACATTTGACGAGACAGAGTACCATGACAGAT 2640
Qy 653 ----- 653
Db 2641 GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATCTTCGCGCGGCTTACCC 2700
Qy 653 ----- 653
Db 2701 CACCAGAGTGTGTGGAGTTATGGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCC 2760
Qy 653 ----- 653
Db 2761 AAACCTTACGATGGATCCAGCCCGGAGATCCCTGACTGTGGTGAAGGGGAGCGG 2820
Qy 653 ----- 653
Db 2821 CTGCCCCAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGTTCAATGTTGGATG 2880

Qy 653 ----- 653
Db 2881 ATTGACTCTGAATGTGCGCAAGATTCCGGAGATGGTGTCTCGAATTTCTCCCGCATGGCC 2940
Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGGACCCCGAGCGCTTTGTGTGTCATCCAGATGAGGACTTGGGCCCGAGCAGTCCCTTG 3000
Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGCACTTCTACCGCTCACTGCTGGAGGACGATGATCGGGGACCTGTGTGGATGCT 3060
Qy 685 GluGluTyrLeuValProGlnGlnGlyPheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGTATACCCAGCAGGGCTTCTTCTGTCCAGACCTCTGCCCGCGCTGGG 3120
Qy 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyAspLeuThr 724
Db 3121 GGCATGCTCCACCACGACGACCGAGCTCTACTACGAGGAGTGGCGGTGGGACCTTGACA 3180
Qy 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3181 CTAGGCTGGAGCCCTCTGAAGAGGAGGCCCTCAGGTCTTCCACTGGCACCTCCGAAGGG 3240
Qy 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
Db 3241 GCTGGCTCCGATGTATTTGATGGTGACCTGGGAATGGGGGCGAGCCAAAGGGCTGCAAGC 3300
Qy 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 3301 CTCCCAACACATGACCCCGAGCCCTCTACAGCGGTACAGTGGAGACCCACAGTACCCCTG 3360
Qy 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3361 CCTCTGAGACTGATGGCTAGCTTGGCCCCCTGACCTGCAGCCCCCAGCTGCAATATGTG 3420
Qy 805 AsnGlnProAspValArgProGlnProSerProArgGluGlyProLeuProAlaAla 824
Db 3421 AACCCAGCAGATGTTGGCCCCCGAGCCCCCTTGGCCCCGAGAGGGGCCCTCTGGCTGTCTGC 3480
Qy 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3481 CGACTGTGTGTGCACTCTGGAAGGGCCAGACTCTCTCCAGGGAGAGATGGGGTCTC 3540
Qy 845 ValLysAspValPheAlaPheGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3541 GTCAAGAGCTTTTGTGCTTTGGGGTGCCTGGGAGAACCCCGAGTACTTGACACCCAG 3600
Qy 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspLeu 884
Db 3601 GGAGGAGTGCCTCTCAGCCCCACCTCTCTCTGCTTTGAGCCCGAGCTTCGACACCTC 3660
Qy 885 TyrTyrTyrAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3661 TATTACTGGGACAGGACCCACAGAGCGGGGGCTTCCACCGAGCACCTTCAAGGGGACA 3720
Qy 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3721 CCTACGCGAGAGAACCCAGAGTACCTGGGTCTGGAGCTGCCAGTG 3765

RESULT 7

US-08-229-515A-9
; Sequence 9, Application US/08229515A
; Patent No. 5518885
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARFAR, FAZLUL H
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200

CITY: Atlanta
 STATE: Georgia
 COUNTRY: usa
 ZIP: 30303
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/229,515A
 FILING DATE: 19 APR 1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: PERRYMAN, DAVID G
 REGISTRATION NUMBER: 33,438
 REFERENCE/DOCKET NUMBER: 1414,608
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-688-0770
 TELEFAX: 404-688-9880
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4530 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-229-515A-9

Alignment Scores:
 Pred. No.: 0 Length: 4530
 Score: 4892.00 Matches: 918
 Percent Similarity: 73.15% Conservative: 0
 Best Local Similarity: 73.15% Mismatches: 1
 Query Match: 96.34% Indels: 336
 DB: 1 Gaps: 1

US-09-493-480-6 (1-919) x US-08-229-515A-9 (1-4530)

181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysAla	200
691	CTCACATGATAGACACCAACCGCTCTCGGGCGCTGCACCCCTGTTCTTCGATGTGTAA	750
201	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220
751	GGCTCCCGCTGCTGGGGAGAGATTCTGAGGATTGTTCAGAGCCTGACGGCACTGTCTGT	810
221	AlaGlyGlyCysAlaArgCysGlyGlyProLeuProThrAspCysCysHisGlnGlnCys	240
811	GCCGGTGGCTGTGCCCGCTGCAAGGGGCCACTGCCCACTGACTGCTGCCATGAGCAGTGT	870
241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
871	GCTGCCGGCTGCAGGCGCCCAAGCACTCTGACTGCTGCGCTGCGCTTCCACTTCAACCAC	930
261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280
931	AGTGGCATCTGTGAGCTGCACCTGCCAGCCCTGGTCACCTACCAACACAGACAGTGTGAG	990
281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300
991	TCCATGCCCAATCCCGAGGCGCGTATACATTCGGCGCCAGCTGTGTGACTGCTGTGCC	1050
301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
1051	TACAACTACCTTTCTACGGAGCTGGGATCCTGCACCTCTGTGCGCCCTTGCACACCAA	1110
321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340
1111	GAGGTGACAGCAGAGGATGGACACACAGCGGTGTGAGAAGTGCAGCAAGCCTCTGCCCGA	1170
341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
1171	GTGTGCTATGGTCTGGGCATGGAGCACTTTCGAGAGGTGAGGGCAGTTACCACTGCCAAT	1230
361	IleGlnGluPheAlaGlyCysValIlePheGlySerLeuAlaPheLeuProGluSer	380
1231	ATCCAGGAGTTTGTGGCTGCAAGAGATCTTTGGAGGCTTGCATTTCTGCCGAGAGC	1290
381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400
1291	TTTGATGGGACCCAGCCTCCAACTGCCCCGCTCCAGCAGCAGCAGCTCCAAGTGTGT	1350
401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro	420
1351	GAGACTCTGGAAGAGATCAAGGTTACCTATACATCTCAGCATGGCGGACAGCCTGCCT	1410
421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyVala	440
1411	GACCTCAGCGCTTTCAGAACCTTGCAGTAATCCGGGACGAATTTCTGCACATGGGCCC	1470
441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
1471	TACTCGTCACTGCAAGGCTGGCATCAGCTGGCTGGGCTGGCTCCTCCTCAGGGAA	1530
461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480
1531	CTGGGAGTGGAGTGGCGCTCATCCACCAATACACCCACCTCTGCTGCTGTCACACCGGT	1590
481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
1591	CCCTGGGACAGCTCTTTGGAAACCCGACCAAGCTCTGCTCCACACTGCGCAACCGGCCA	1650
501	GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
1651	GAGGACAGTGTGTGGCGAGGCGCTGGCGCTGCACCGCTGTGGCGCCGAGGGCACTGC	1710
521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
1711	TGGGGTCCAGGGGCCCACTGATGTGTCACTGACAGCAGTGTCTTCTCGGGGCGCAGAGTGC	1770

QY 541 valGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaAraGHisCys 560
DB 1771 GTGGAGGAATGCCAGTACTGCGAGGGCTCCCCAGGGAGTATGTGAATGCCAGGCACTGT 1830
QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
DB 1831 TTGCGGTGCACCTCTGAGTGTGAGCCCGCCAGATGGCTCACTGACCTGTCTTTGGACCGGAG 1890
QY 581 AlaAspGlnCysValAlaCysAlaHisTyrIlyAspProProPheCysValAlaAraGHisCys 600
DB 1891 GCTGACCAAGTGTGGCTGTGGCCCACTATAAGGACCTCCCTTCTCGTGGCGCGCTGC 1950
QY 601 ProSerGlyValIlyProAspLeuSerTyrMetProIleTyrPhePheProAspGluGlu 620
DB 1951 CCAGCGGTGTGAACCTGACCTCTCTTACATGCCCATCTGGAAGTTTTCAGATGAGGAG 2010
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
DB 2011 GGGCGATGCCAGCTTGGCCCATCACTGACCCACTCTCTGTGTGGACCTGGATGACAAG 2070
QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
DB 2071 GGCTGCCCGCCGAGCAGAGAGCCAGCCCTCTGACGTCCATCGTCTCTGGGGTGGTTGGC 2130
QY 653 ----- 653
DB 2131 ATTCTGCTGCTGCTGTGTTGGGGTGGTCTTTGGGATCTCTCATCAAGCGACGGCAGAG 2190
QY 653 ----- 653
DB 2191 AAGATCCGGGAAGTACAGATGCGGAGACTGCTGCGAGGAACGGAGCTGGTGGAGCCGCTG 2250
QY 653 ----- 653
DB 2251 ACACCTAGCGGAGCGATGCCCAACAGCGCGAGATGCGGATCTCTCATCAAGCGACGGAGCTG 2310
QY 653 ----- 653
DB 2311 AGGAAGTGAAGTGTGTTGGATCTGGGCTGTTGGGCACAGTCTTCAAGGGGATCTGGATC 2370
QY 653 ----- 653
DB 2371 CCTGATGGGGAGATGTGAATAATTCAGTGGCCATCAAGTGTGAGGGAAAAACATATCC 2430
QY 653 ----- 653
DB 2431 CCCAAGCCAAACAGAAATCTTAGACGAATACATGATGCTGGTGGGCTCCCA 2490
QY 653 ----- 653
DB 2491 TATGCTCTCCGCTTCTGGGCACTGCTGATCATCAAGTGCAGCTGGTGACACAGCTT 2550
QY 653 ----- 653
DB 2551 ATGCCCTATGCTGCTCTTAGACCATGTCCGGGAACCCGGAGCGCTGGGCTCCGAG 2610
QY 653 ----- 653
DB 2611 GACCTGTGAATGCTGTATGCAATGTCGAAGGAGTACCTACCTGGAGGATGTGCGG 2670
QY 653 ----- 653
DB 2671 CTCGTACACAGGAGCTTGGCGCTCGGAACGTGCTGATCAAGAGTCCCAACCATGTCAAA 2730
QY 653 ----- 653
DB 2731 ATTACAGACTTTCGGGTGGCTCGGCTGTGACATTTGACGACAGAGATCAATGCAGAT 2790
QY 653 ----- 653
DB 2791 GGGGGCAAGTGGCCCATCAAGTGGATGGCGCTGGAGTGCATTTCTCCGCGCGGCTTACCC 2850
QY 653 ----- 653

RESULT 8

US-08-645-865-9

DB 2851 CACCAGAGTGTGTGTGGAGTTATGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCC 2910
QY 653 ----- 653
DB 2911 AAACCTTACGATGGATCCAGCCCGGAGATCCCTGACCTGTCTGGAAGGGGGAGCGG 2970
QY 653 ----- 653
DB 2971 CTGCCCCAGCCCCCATCTGTGCACCAATTGATGTCTACATGATCAATGGTCAATATGTTGGATG 3030
QY 653 ----- 653
DB 3031 ATTGACTCTGAAATGTCCGCCAAGATTCCGGAGTTGGTGTCTGAATTTCTCCCGCATGCCC 3090
QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
DB 3091 AGGACCCCGCCAGCGCTTTGTGTCTATCCAGAAATGAGGACTTGGGCCCGACGAGTCCCTTG 3150
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
DB 3151 GACAGCACCTTCTACCGCTCACTGTGGAGACGATGATGAGGGGACTGTGTGATGCT 3210
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
DB 3211 GAGGATATCTGTATCCCGACGAGCGCTTCTTCTGTCCAGACCTGCCCCGGCGCTGG 3270
QY 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
DB 3271 GGCAATGCTCCACACAGCACCGCAGCTCTATACAGAGTGGCGGTGGGGACCTGACACA 3330
QY 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
DB 3331 CTAGGGTGGAGCGCTCTGAAGAGAGAGCCCCAGGTCTCCACTGGCACCTCCGAGGG 3390
QY 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
DB 3391 GCTGGCTCCGATATTTGATGTGACTGGGAATGGGGCAGCAAGGGCTGCAAGC 3450
QY 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
DB 3451 CTCCCCACATGATCCCGACCGCTCTACAGCGGTACAGTGGAGGCCACACAGTACCCCTG 3510
QY 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
DB 3511 CCCTCTGAGACTGATGGCTAGTGTGCCCTGACCTGACCTGACGCCCGACCTGATATGTG 3570
QY 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
DB 3571 AACCCAGCCAGATTTCCGCCCGCCAGCCCTTCCGCCCGAGAGGGCCCTCTGCTGCTGCC 3630
QY 825 ArgProAlaGlyAlaThrLeuGluArgProIlyThrLeuSerProGlyIlyAsnGlyVal 844
DB 3631 CGACTGTGTGTGCACTCTGGAAGGGCCAGAGCTCTCTCCCGAGGAAGAAATGGGGTC 3690
QY 845 ValIlyAspValPheAlaPheGlyAlaValGluAsnProGluTyrLeuThrProGln 864
DB 3691 GTCAGACGCTTTTGTCTTTGGGGTGTGGTGGAGAACCCCGAGTACTTGACACCCAG 3750
QY 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
DB 3751 GGAGGAGTGGCCCTCAGCCCCCACCCTCTCTGCTTTCAGCCCGACGCTTCGACCACTC 3810
QY 885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheIlyGlyThr 904
DB 3811 TATTACTGGACCAAGGACCCAGAGCGGGGCTCCAGCCAGCAGCTTCAAGAGGACA 3870
QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
DB 3871 CCTACGGCAGAGAACCCAGAGTACTGTGGTCTTGGACGCTGCCAGTG 3915

Sequence 9, Application US/08645865
Patent No. 5654406
GENERAL INFORMATION:
APPLICANT: RAZIUDIN
APPLICANT: SARKAR, FAZLUL H
TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPlastic DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,865
FILING DATE: 14 MAY 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414,608
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
TELEFAX: 404-688-9880
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4530 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-645-865-9

Alignment Scores:
Pred. No.: 0 Length: 4530
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 1 Gaps: 1

US-09-493-480-6 (1-919) x US-08-645-865-9 (1-4530)

QY 1 MetGluLeuAlaLeuCysArgTrpGlyLeuLeuAlaLeuLeuProProGlyAla 20
DB 151 ATGGAGCTGGCGCCTTGTGGCGCTGGGGGCTCTCTCGCCCTCTTGGCCCCCGAGCC 210
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
DB 211 GCGAGCACCAGTGTGACCGGCGACGACATGAGCTGGGCTCTCTCGCCAGTCCCGAG 270
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
DB 271 ACCACCTGGACATGCTCCGCCACCTCTACCGGGCTGCCAGTGTGGTGGCGAAACCTG 330
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
DB 331 GAACCTCACCTAGCTGCTATGCTTCAACCAAGTGGAGCGAGTCCCACTGCAGAGGCTGCG 390
QY 81 GlnGlyTyrValLeuIleAlaHisGlnGlnValArgGlnValProLeuGlnArgLeuArg 100
DB 391 CAGGGCTAGCTGCTATGCTTCAACCAAGTGGAGCGAGTCCCACTGCAGAGGCTGCGG 450
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
DB 451 ATTGTGGAGGACCCAGCTCTTTGAGGACAACTATGCTTGGCGCTGTAGACATGGA 510

QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
DB 511 GACCCGCTGAACAATACCAACCCCTGTCTACAGGGGCTCCCCAGGAGGCTGGGGAGCTG 570
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuLeuIleGlnArgAsnProGln 160
DB 571 CAGCTTCGAGCCTCACAGAGATCTTGAAGAGGGGTCTTGATCCAGCGGAACCCAG 630
QY 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnGlnLeuAla 180
DB 631 CTCTGCTACCAAGACACGATTTGTGAAGGACATCTTCCACAGAACCAACAGCTGGCT 690
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
DB 691 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTCTCGATGTGTA 750
QY 201 GlySerArgCysTrpGlyLysSerGluAspCysGlnSerLeuThrArgThrValCys 220
DB 751 GCTCCCGCTGCTGGGGAGAGAGTTCTGAGGATTCAGAGCTTCAGCGGCACTGTCTGT 810
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
DB 811 GCCGCTGGCTGTGCCCGCTGCAAGGGGCGACTGCCACTGCTGCTGCCATGAGCAGTGT 870
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
DB 871 GCTGCCGCTGCACGGGCCCCAGCACTCTGACTGCTGCTGCTGCTGCTGCTGCTGCTG 930
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
DB 931 AGTGGCATCTGTGAGCTGCACCTGCCAGCGCTGGTCCCTACCAACACAGACAGTTTGA 990
QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
DB 991 TCCATGCCCAATGCCGCGCGGTATACATTGGCGCGCAGCTGTGTGACTGCTGCTGCC 1050
QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
DB 1051 TACAACCTACTTCTACGAGCTGGGATCTGCACCTGCTGCTGCCCTGCAACACCA 1110
QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
DB 1111 GAGGTGACAGCAGAGAGATGGAACACAGCGCTGTGAGAGTGCAGCAAGCCCTGTGCC 1170
QY 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
DB 1171 GTGTCTATGCTGTGGCATGGAGCACTTGGCAGAGGTGAGGGCAGTTACCACTGCAAT 1230
QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
DB 1231 ATCCAGGAGTTTGTGGCTGCAAGAGATCTTGGGAGCTGGCACTTCTGCCGAGAGC 1290
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe 400
DB 1291 TTTGATGGGAGCCAGCTCCCAACACTGCCCGCTCCAGCAGAGCAGCTCCCAAGTGT 1350
QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
DB 1351 GAGACTCTCGAGAGATCAGGTACCTATATCTACGATGGCGCGGACAGCTGCTCT 1410
QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
DB 1411 GACCTCAGGCTCTTCCAGAACCTGCAAGTAATCCGGGAGCAATTTGACACATGGGCC 1470
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuArgSerLeuArgGlu 460
DB 1471 TACTCGCTGACCTGCAAGGGCTGGGCATCAGCTGCTGGGCTGGGCTGCTGCTGCTG 1530
QY 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
DB 1531 CTGGGAGGTGGAGTGGCGCTCTATCCACCAACCCACCTCTGCTGCTGCTGCTGCTG 1590
QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500

QY 885 TTTTtTtPAspGlnAspProProGluArgGlyAlaProProSerThrPhelysGlyThr 904
Db 3811 TATTACTGGACACAGGACCCACAGAGCGGGGGCTCCACCCAGACACCTTTCAAGGGGACA 3870
QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3871 CCTACGGCAGAGAACCCAGAGTACTCTGGGTCTGGAGCTGCCAGTG 3915

RESULT 9

US-09-167-322-4
; Sequence 4, Application US/09167322
; Patent No. 6365151
; GENERAL INFORMATION:
; APPLICANT: Allegheny University of the Health
; Sciences, James M.
; England, Halpern, Michael S.
; TITLE OF INVENTION: CANCER VACCINE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seigel, Gonda, Lavorgna & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/167,322
; FILING DATE: 07-Oct-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/00582

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 7933-33 PC

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 4530 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-167-322-4

Alignment Scores:
Pred. No.: 0 Length: 4530
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 4 Gaps: 1

US-09-493-480-6 (1-919) x US-09-167-322-4 (1-4530)

QY 1 MetGluLeuAlaAlaLeuCysArgTTPGlyLeuLeuLeuAlaLeuLeuProProGlyAla 20
Db 151 ATGGAGCTGGGGCTTGTGCGCTGGGGCTCTCTCTGCGCTCTTGGCCCTTGGCCCGGAGCC 210
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 211 GCGAGCACCCAGTGTGCACCGGCACAGACATGAAGCTGGGGCTCTCTGCGCTCTTGGCCCGGAG 270
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60

Db 271 ACCACCTGGACATGCTCGCCACCTCTACAGGGCTGCGAGGTGTGCGAGGAAACCTG 330
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnPheLeuVal 80
Db 331 GAACTCACCTACCTGCGCCCAATGCAGCTGTCTCTCTGAGGATATCCAGGAGGTG 390
QY 81 GlnGlyTyrValLeuLeuAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 391 CAGGGCTACGTCTCATCGCTCACACCAAGTGAGGCGAGTCCCACTGCGAGAGCTCGG 450
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 451 ATTTGCGAGGACCCAGCTCTTTGAGGACCACTATGCTCCCTGCGCTGTAGCAATGGA 510
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 511 GACCCGCTGAACAATACCACTCTGTCAGAGGGGCTCTCCAGAGGCTTGGCGAGCTG 570
QY 141 GlnLeuArgSerLeuThrGluLeuLeuLysGlyValLeuLeuIleGlnArgAsnProGln 160
Db 571 CAGCTTCGAGGCTTCACAGAGATCTTGAAGGAGGGCTCTTGATCCAGCGGAAACCCCG 630
QY 161 LeuCysTyrGlnAspThrIleLeuThrLysAspIlePheHisLysAsnGlnLeuAla 180
Db 631 CTCTGCTACAGGACACGATTTGTGGNAGGACATCTTCCACAAGAACAAACCACTGGCT 690
QY 181 LeuThrLeuLeuAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 691 CTCACACTGATAGACACCAACCGCTCTCGGGCTTCCACCCCTGTTCTCGATGTGTAA 750
QY 201 GlySerArgCysTTPGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 751 GAGCTCCCGCTGCTGGGGAGGAGATTCTGAGGATTGTTCAGAGCTTGCAGCGCACTGT 810
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
Db 811 GCGGTGGCTGTGCTCGCTGCAAGGGGCCACTGCCACTGCTGCTGCCATGACAGTGT 870
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 871 GCTGCGGGCTGCGCGGGCCCAAGCACTCTGAGCTGCTGCGCTGCCCTCCACTTCAAC 930
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 931 AGTGGCATCTGTGAGCTGCACTGCCCGAGCCCTGTGTCACTTACAACACAGACACG 990
QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 991 TCCATGCCCAATCCCGAGGGCCGGTATACATTCGGCGCCAGCTGTGTGACTGCTGTCCC 1050
QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db 1051 TACAACCTACCTTCTACGGAGCTGGGATCTCTGCACCTCTGCTGCTGCTGCTGCTGCT 1110
QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
Db 1111 GAGGTGACACGACGAGGATGGAACACACGCGGTGTGAGAAGTGCAGAGAGCCCTGTG 1170
QY 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
Db 1171 GTGTGCTATGCTTGGGCACTTGGGACATGGGACATCTGGAGAGGTGAGGGCAGATTAC 1230
QY 361 IleGlnGluPheAlaGlyCysLysValPhePheGlySerLeuAlaPheLeuProGluSer 380
Db 1231 ATCCAGAGGTTCCTGGCTGCAAGAGATCTTTGGGAGCTTGGCATCTTCTGCGGAGAG 1290
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
Db 1291 TTTGATGGGAGCCAGGCTCCACACTGCTCCCGCTCCAGCGCAGAGCAGCTCCAAGTGT 1350
QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTTPProAspSerLeuPro 420

1351	Db	GAGACTCTGGAGAGATCATCAGGTTACCTATATCATCTGAGCATGGCGGACAGACCTGGCT	1410
421	Qy	AspLeuSerValPheGlnAsnLeuGlnValIleAargGlyVargIleLeuHisAsnGlyAla	440
1411	Db	GACCTCAGCGCTCTCCAGAACCTGCAAGTAATCCGGGGAGCAATCTCGCACAAATGGCGCC	1470
441	Qy	TyrSerLeuThrLeuGlnGlnGlyLeuGlyIleSerTrpLeuGlyLeuAargSerLeuAargGlu	460
1471	Db	TACTCGCTGACCTCGCAAGGCGCTGGGCATCAGCTGGCTGGGGCTGGCGCTACTGAGGGAA	1530
461	Qy	LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal	480
1531	Db	CTGGGCAGTGGACTGGCGCTCATCCACCAATACCCCACTCTGCTTGTGTGCACAGGTG	1590
481	Qy	ProTrpAspGlnLeuPheAargAsnProHisGlnAlaLeuLeuHisThrAlaAsnAargPro	500
1591	Db	CCCTGGGACCAAGCTCTTTGGAAACCCGCACCAAGCTCTGTCTCCACACTGCCAACCCGCCA	1650
501	Qy	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaAargGlyHisCys	520
1651	Db	GAGGACGAGTGTGTGGCGAGGGCGCTGGCGCTGCCACCACTGTGTGCGCCGAGGGCACTGC	1710
521	Qy	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuAargGlyGlnGluCys	540
1711	Db	TGGGGTCCAGGGCCACCCAGTGTGTCACTGCAGCCAGTCTCTTGTGGGGCCAGGAGTGC	1770
541	Qy	ValGluGluCysAargValLeuGlnGlnLeuProAargGluTyrValAsnAlaAargHisCys	560
1771	Db	GTGAGGAAATGCCAGTACTTCGAGGGGCTTCCGAGGGAGTATGTGAATGCCAGGCACTGT	1830
561	Qy	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
1831	Db	TTGCGGTGCCACCTGTAGTGTTCAGCCCCAGAAATGGCTCAGTGACCTGTTTTGGACGGAG	1890
581	Qy	AlaAspGlnCysValAlaCysAlaHisTyrIlyAspProProPheCysValAlaAargCys	600
1891	Db	GCTGACCAGTGTGTGGCGCTGTGCCCACTATAAGAGACCTCTCCCTCTGCGTGGCGCCGCTGC	1950
601	Qy	ProSerGlyValIlyProAspLeuSerTyrMetProIleTrpIlyPheProAspGluGlu	620
1951	Db	CCGAGCGGTGAAACCTGACCTCTCTCATATGCCCACTTGGAAAGTTTCCAGATGAGAG	2010
621	Qy	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640
2011	Db	GGCGATCGCAGCCTTGCCCCATCACTGCACCCCACTCTCTGTGTGACCTTGGATGACAAG	2070
641	Qy	GlyCysProAlaGluGlnAargAlaSerProLeuThrSer	653
2071	Db	GGCTGCCCCGCGAGCAGAGACCGCCCTCTGACGTCCATCGTCTCTGCGGTGGTGGC	2130
653	Qy	-----	653
2131	Db	ATTCTGTGTGTGTGTCTTGGGGGTGTCTTTGGGATCTTCATCAGCGCAGCGCAGCAG	2190
653	Qy	-----	653
2191	Db	AAGATCCGGAAGTACACGATGCGGAGACTGTCTGCAGGAAACCGGAGCTGTGTGAGCCGCTG	2250
653	Qy	-----	653
2251	Db	ACACTAGCGGAGCGATGCCCAACCGAGCGCAGATGCGGATCTCTGAAGAGACGAGCTG	2310
653	Qy	-----	653
2311	Db	AGGAAGGTGAAGTGTCTTGGATCTGGCGCTTTTGGCAGCTCTACAGGGCATTCTGGATC	2370
653	Qy	-----	653
2371	Db	CCTGATGGGAGAAATGTGAANAATTCAGTGGCCCATCAAGTGTGTGAGGGGAAACACATCC	2430
653	Qy	-----	653
2431	Db	CCCAAGCCAAACAAAGAAATCTTAGACGAAGCATACGTGTATGGCTGTGTGTGGCTCCCCA	2490

Db 3691 GTCAAGACGTTTGTGGGCTGGGAGAACCCCGAGTACTTGACACCCCCAG 3750
Qy GlyGlyAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3751 GGAGAGCTGCCCTCAGCCCAACCTCTCTGCTTCAGCCCGAGCTTCGACACCTC 3810
Qy TyrTyrTrpAspGlnAspProGluArgGlyAlaProProSerThrPheGlyThr 904
Db 3811 TATTACTGGACAGGACCAACAGAGCGGGGGCTCCACCCAGCACCTTCAGAGGGACA 3870
Qy ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3871 CCTACGGCAGAGAACCCAGAGTACTGGGCTCGGACGTGCCAGTG 3915

RESULT 11

US-09-877-177A-11
; Sequence 11, Application US/09877177A

; Patent No. 6582919

; GENERAL INFORMATION:

; APPLICANT: K. Danenberg

; TITLE OF INVENTION: Method of determining Epidermal Growth

; TITLE OF INVENTION: Factor Receptor and HER2-Neu Gene Expression

; TITLE OF INVENTION: and Correlation of Levels Thereof With Survival

; FILE REFERENCE: 11220/120

; CURRENT APPLICATION NUMBER: US/09/877,177A

; CURRENT FILING DATE: 2001-06-11

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 11

; LENGTH: 4530

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-877-177A-11

Alignment Scores:

Pred. No.: 0 Length: 4530
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 4 Gaps: 1

US-09-493-480-6 (1-919) x US-09-877-177A-11 (1-4530)

Qy 1 MetGluLeuAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
Db 151 ATGGAGCTGGCGGCTTGTGCGCTGGGGCTCTCTCGCCTCTTGCCCGCGAGCC 210
Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 211 GCGAGCACCCAAAGTGTGCACCGGCACACATGAAGCTGGGCTCCCTGCCAGTCCCGAG 270
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 271 ACCCACTGGACATCTCGGCACCTCTACACAGGGCTGCCAGGTGGTGGAGGAAACCTG 330
Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 331 GAACTCACTACTGCGCCACCAACATGCCAGGCTGCTCTTCTGCAGGATATCCAGGAGTG 390
Qy 81 GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 391 CAGGCTACGTGCTCATCGCTCACAAACCAAGTGGAGGAGGTGCCACTGCGAGGGCTGCGG 450
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 451 ATTGGCGGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGCTGCTAGCAATGGA 510
Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyLeuArgGluLeu 140
Db 511 GACCCGCTGAACAATACCAACCTCTGTCAAGGGGCTCCCGAGGAGGCTGCGGAGCTG 570

Qy 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgSerProGln 160
Db 571 CAGCTTCGAGCCCTCACAGATCTTGAAGAGAGGGTCTTGATCCAGCGGAACCCCCAG 630
Qy 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLeuAsnAsnGlnLeuAla 180
Db 631 CTCTGCTACAGGACAGATTTTGTGGAAGGACATCTTCCACAGACAAACACAGCTGGCT 690
Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 691 CTCACACTGATAGACACCAACCGCTCTCGGCGCTGCCACCCCTGTTCTCCGATGTGTAAG 750
Qy 201 GlySerArgCysTrpGlyLysSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 751 GGCTCCCGCTGCTGGGGAGAGATTTCTGAGGATTTGTGAGAGCTTCAGCGGCACTGTCTGT 810
Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
Db 811 CCGGTGCTGTGCTGCTGCAAGGGGCACTGCCCACTGACTGTCTGCCATGAGCAGTGT 870
Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 871 GCTGCCGCTGCACGGGCCCCAAGCACCTCTGACTGCTGCTGCTGCCCTGCCCTTCAACCCAC 930
Qy 261 SerGlyIleCysGluLeuHisCysProAlaValThrTyrAsnThrAspThrPheGlu 280
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Qy 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 991 TCCATGCCCAATCCCGAGGGCGGTATACATTCGGGGCCAGCTGTGTGACTGCTGTCCC 1050
Qy 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db 1051 TACAACCTACTTTCTACGGAGCTGGGATCTCTGCACCTCTGCTGCCCTTGCACCAACCAA 1110
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Db 1111 GAGGTGACAGCAGAGGATGGAAACACACGCGTGTGAGAGTGGACNAGCCTGTGCGCCGA 1170
Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
Db 1171 GTGTCTATGCTTGGGCAATGGAGCACTTTCGAGAGGTGAGGGCAGTTACCACTGCTCAAT 1230
Qy 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 1231 ATCCAGGAGTTTGTCTGGCTGCAGGAAGATCTTTTGGAGGCTGGCATTTCTGCGGAGAGC 1290
Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
Db 1291 TTTGATGGGAGCCCGAGCTCCAACTGCCCGCTCCAGCCAGAGCAGCTCCCAAGTGT 1350
Qy 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
Db 1351 GAGACTCTGGAAGAGATCACAGTTTACCTATACATCTCAGCATGCGCGAGCAGCTGCTC 1410
Qy 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisGlnGlyAla 440
Db 1411 GACCTCAGCGCTTCCAGAACCTGCAAGTAATCCGGGAGCAATTTCTGCACAAATGGGCC 1470
Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
Db 1471 TACTCGCTGACCTCCAGGGCTGGGCATCAGCTGGCTGGGCTGGGCTCCTCAGTGGGAA 1530
Qy 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
Db 1531 CTGGGCGAGTGGACTGGCTCATCCACCATACACCCACTCTGCTGTCTGTCGACACAGGTG 1590
Qy 481 ProTrpAspGlnLeuPheAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
Db 1591 CCCTGGGACAGCTCTTTTGGAAACCGCACCAAGCTCTCTCTCAGCTCTGCTCCAAACCCGCCA 1650
Qy 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520

Db	1651		GAGGACAGGTGTGTGGCGAGGGCTTGGCTGCACCAGCTGTGTGGCCCGAGGGCACTGC	1710
Qy	521		TriGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
Db	1711		TGGGGTCCAGGGGCCACCCAGTGTGTCACTGCAGCCAGTTCCTTCGGGGCCAGGAGTGC	1770
Qy	541		ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560
Db	1771		GTGAGAGNATGCCAGTACTGCAGGGGCTCCCCAGGGAGTATGTGTGAATGCCAGGCATGT	1830
Qy	561		LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
Db	1831		TTGCGGTGCCACCTTGAGTGTACCCCGAGATGGCTCAGTGACCTGTTTTGACCGGAG	1890
Qy	581		AlaAspGlnCysValAlaCysAlaHisIleTyrIleAspProPheCysValAlaArgCys	600
Db	1891		GCTGACAGTGTGTGGCTGTGTGCCACTATAGGAGCCCTCCCTTCGTGGCCCGCTGC	1950
Qy	601		ProSerGlyValIysProAspLeuSerTyrMetProIleTyrIlePheProAspGluGlu	620
Db	1951		CCGACGGGTGTGAACCTGACCTCTCTACATGCCCATCTGGAGGTTCAGATGAGGAG	2010
Qy	621		GlyValaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspIys	640
Db	2011		GGCGATGCCAGCTTGGCCCATCACTGCACCCACTCTCTGTGTGGACCTGGATGACAG	2070
Qy	641		GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
Db	2071		GGCTGCCCCCGGAGCAGAGAGCCAGCCCTCTGACGTCCATCGTCTCTCGGTGGTGTGGC	2130
Qy	653	----	-----	653
Db	2131		ATTCTGTGTGTGTGTCTTGGGGGTGGTCTTTGGGATCTCTATCAGCGACGGCAGCAG	2190
Qy	653	----	-----	653
Db	2191		AAGATCCGGAAGTACACGATCGGAGACTGCTGCAGGAACCGAGCTGTGTGGAGCCGCTG	2250
Qy	653	----	-----	653
Db	2251		ACACTAGCGGAGCGATGCCCAACCGCGCGAGATCGGGATCTCTGAAGAGACGGAGCTG	2310
Qy	653	----	-----	653
Db	2311		AGGAAGGTGAAGGTGTGTGGATCTGGCGCTTTTGGCACAGTCTACAGGGCATCTGGATC	2370
Qy	653	----	-----	653
Db	2371		CCTGATGGGGAGATGTGAATAATTCAGTGGCCATCAAGTGTGTGAGGGGAAACACATCC	2430
Qy	653	----	-----	653
Db	2431		CCCAAGCCCAACAGAAATCTTAGACGAAGCATACGTGATGGCTGTGTGGGCTCCCCA	2490
Qy	653	----	-----	653
Db	2491		TATGTCTCCGCGCTCTTGGGCGATCTGCTTGACATCCACGGTGCAGCTGTGTGACACAGCTT	2550
Qy	653	----	-----	653
Db	2551		ATGCCCTATGGCTGCTCTTTAGACCATGTCCGGGAAACCGCGSACGCTGGGCTCCAG	2610
Qy	653	----	-----	653
Db	2611		GACCTGCTGAATGGTGTATGCAGATTGCCAAGGGATGAGCTACCTGGAGGATGTGGG	2670
Qy	653	----	-----	653
Db	2671		CTCGTACACAGGAGCTTGGCGGCTCGGAAGTGTGTGTCAAGAGTCCCAACCATGTCAAA	2730
Qy	653	----	-----	653

2731	ATTA	CAGACTTCGGGCTGGCTCGGCTGCTGGA	CAATTGACGAGACAGAGTACCATGCAGAT	2790
653	QY	-----	-----	653
2791	GGGG	CAAGGTGCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCGCGGCTTCACC	2850	
653	QY	-----	-----	653
2851	CAC	CAGAGTCAATGTGTGGAGTTATGTGTGCACTGTGTGGGAGCTGATGA	CTTTTGGGGCC	2910
653	QY	-----	-----	653
2911	AAAC	TTACGATGGGATCCCGAGCCGGGAGATCCCTGACCTGTCTGGAAAAGGGGAGCGG	2970	
653	QY	-----	-----	653
2971	CTG	CCCCAGCCCCCATCTGCACCAATTGATGTCTATCATGATCATGTGTCAAATTTGGATG	3030	
653	QY	-----	-----	653
3031	ATT	GACTCTGAATGTGGGCCAAGATTCGGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC	3090	
654	QY	-----	-----	654
3091	AGG	ACCCCGCAGCGCTTTGTGTGTCATCCAGATGAGGACTCTGGCGCCAGCCAGTCCCTTG	3150	
665	ASP	SerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla	684	
3151	GAC	AGCACCTTCTACCGCTCACTGTCTGGAGAGATGACATGGGGACCTTGGTGGATGCT	3210	
685	GLU	GLuTyrLeuValProGLinGLinGlyPhePheCysProAspProAlaProGlyAlaGly	704	
3211	GAG	AGTATCTGTATACCCAGCAGGGCTTCTTCTGTCCAGACCTTGCCCCGGGCGCTGGG	3270	
705	GLY	MetValHisArgHisArgSerSerSerThrArgSerGlyGlyGlyAspLeuThr	724	
3271	GGC	ATGTTCCACACAGGCACCGCAGCTCATCTACCAGGAGTGGCGTGGGACCTTGACA	3330	
725	LEU	GLyLeuGLuProSerGLuGLuAlaProArgSerProLeuAlaProSerGLuGly	744	
3331	CTA	GGGCTGGAGCCCTCTGAAAGAGAGGCCCCACAGGTCTCCATGGCACCTCTCGAAGGG	3390	
745	ALG	LYSerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaIysGlyLeuGLinSer	764	
3391	GCT	GGCTCCCATGATTTGATGTGACCTCTGGGAATGGGGCAGCCAAAGGGGCTGCAAGC	3450	
765	LEU	ProThrHisAspProSerProLeuGLinArgTyrSerGLuAspProThrValProLeu	784	
3451	CTC	CCCCACATGACCCCGCCCTCTACAGCGGTACAGTGGAGACCCCAAGTACCCCTG	3510	
785	PRO	SerGLuThrAspGlyTyrValAlaProLeuThrCysSerProGLinProGLuTyrVal	804	
3511	CCCT	CTGAGACTCATGCTACGTTGCCCTTCTGACCTGCGAGCCCCCAGCCCTGAATATGTG	3570	
805	ASN	GLinProAspValArgProGLinProProSerProArgGLuGlyProLeuProAlaAla	824	
3571	AAC	CAGCCAGATGTGTGGCCCCCAGCCCCCTTCGCCCGAGAGGGCCCTCTGCTGCTGCC	3630	
825	ARG	ProAlaGLyAlaThrLeuGLuArgProLYsThrLeuSerProGLyLYsAsnGlyVal	844	
3631	CGA	CTCTGCTGGTGGCACTCTGGAAAGGGCCAGACTCTCTCCCCAGGGAAGATGGGGTC	3690	
845	VAL	LYsAspValPheAlaPheGLyGlyAlaValGLuAsnProGLuTyrLeuThrProGLin	864	
3691	GT	CAAGACCGTTTTTGCTTTTGGGGGTGGCGTGGAGAACCCCGAGTACTTGAACCCCGAG	3750	
865	GLY	GLyAlaAlaProGLinProHisProProProAlaPheSerProAlaPheAspAsnLeu	884	
3751	GAG	GGAGCTGCCCTCTAGCCCCACCTCTCTCTCTGCTTCAGCCAGCTTCGACAACTTC	3810	
885	Tyr	TyrTrpAspGLinAspProProGLuArgGLyAlaProProSerThrPheLYsGlyThr	904	
3811	TATT	ACTGGACACGACCCACACAGAGCGGGGGCTCCACCCAGACCTTCAAGGGACA	3870	

Qy 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
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Dp 3871 CCTACGGCAGAGAACCCAGAGATACCTGGGTCTGGACGTGCCAAGTG 3915
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RESULT 12

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US-09-811-115-1
; Sequence 1, Application US/09811115
; Patent NO. 6632979
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT.034A
; CURRENT APPLICATION NUMBER: US/09/811,115
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9274
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Vector Sequence
US-09-811-115-1

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Alignment Scores:					
Pred. No.:	0	Length:	9274		
Score:	4892.00	Matches:	918		
Sent Similarity:	73.15%	Conservative:	0		
Best Local Similarity:	73.15%	Mismatches:	1		
Query Match:	96.34%	Indels:	336		
DG:	4	Gaps:	1		

US-09-493-480-6 (1-919) x US-09-811-115-1 (1-9274)

Qy	1	Met	Glut	Leu	Ala	Ala	Leu	Cys	Arg	Tyr	Gly	Leu	Leu	Leu	Ala	Leu	Leu	Pro	Pro	Gly	Ala	20
Db	1731	AT	GAG	CT	TGG	CGG	CT	TGG	CGG	CT	TGG	CGG	CT	TGG	CGG	CT	TGG	CGG	CT	TGG	CGG	1790
Qy	21	Ala	Ser	Thr	Gln	Val	Cys	Thr	Gly	Thr	Asp	Met	Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	40	
Db	1791	GCG	AGC	ACC	CAAG	TGT	GC	ACG	GAC	AGA	CAT	GA	GAG	CT	TGG	CGG	CT	TGG	CGG	CT	1850	
Qy	41	Thr	His	Leu	Asp	Met	Leu	Arg	His	Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	60
Db	1851	ACC	CAC	CTG	GAC	TGCT	CGG	CAC	CTCT	TAC	CAG	GGCT	GCC	CAG	TGG	TGC	CAG	GAA	ACC	TG	1910	
Qy	61	Glu	Leu	Thr	Tyr	Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	Gln	Leu	80	
Db	1911	GAA	CTC	AC	TAC	CTG	CCC	CAC	CAAT	GCC	CAG	CGCT	GT	CTCT	CTC	TGC	CAG	GATAT	TCC	CAG	1970	
Qy	81	Gln	Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	Val	Arg	Gln	Val	Pro	Leu	Gln	Arg	Leu	100	
Db	1971	CAG	GCT	AC	GGT	CTAT	CGCT	CAC	CA	CC	AGT	GAG	GAG	GCT	TCC	CACT	TGC	CAG	GCT	CGG	2030	
Qy	101	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	Asp	Asn	Tyr	Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly	120
Db	2031	ATT	TG	CGC	GAG	CAC	CC	CAG	CTCT	TTT	GAG	CAC	AAT	TAT	GC	CCCT	TGG	CGGT	GT	CAG	2090	
Qy	121	Asp	Pro	Leu	Asn	Asn	Thr	Thr	Pro	Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	140	
Db	2091	GAC	CGCT	GA	CAAT	TAC	CAC	CCCT	TG	TCA	G	GGG	CCCT	CCC	CAG	GAG	GCCT	TGC	GGG	AGCT	2150	
Qy	141	Gln	Leu	Arg	Ser	Leu	Thr	Glu	Ile	Leu	Gly	Gly	Val	Leu	Ile	Gln	Arg	Asn	Pro	Gln	160	
Db	2151	CAG	CTT	CGA	AGC	CTC	AC	GAT	CTT	GAA	AGG	GGGT	CTT	GT	ATC	TCC	AG	CGG	GA	CCCC	2210	
Qy	161	Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe	His	Tlys	Asn	Asn	Gln	Leu	180	

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QY 541 ValGluGluCysArgValLeuGlnGlyLeuProAArgGluTyrValAsnAlaArgHisCys 560
Db 3351 GTGGAGGAATCGCGAGTACTGCAAGGGGCTCCCGAGGGAGTATGTGAATGCCAGGCACTGT 3410
QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 3411 TTGCCGTGCCACCTCGAGTGTGAGCCCAAGAAATGGCTGAGTGACCTGTTTTTGGACCCGAG 3470
QY 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
Db 3471 GCTGACCACTGTGGCTGTGCGCCACTATAGGACCTCCCTCTCTGCGTGGCCCGCTGC 3530
QY 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu 620
Db 3531 CCACGGGTGTGAACCTGACCTCTCTACATGCCATCTGGAAGTTTCCAGATGAGGAG 3590
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
Db 3591 GGCGCATGCCAGCTTTGCCCATCACTGCACCTCTCTGTGTGACCTGGATGACAAG 3650
QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
Db 3651 GSCTGCCCCCGAGCAGAGACCGCCCTCTGACGTCCATCGTCTCTGCGGTGGTGGC 3710
QY 653 ----- 653
Db 3711 ATTCTGCTGCTGCTGTGGGTGGTCTTTGGGATCCTCATCAAGCGACGACGAG 3770
QY 653 ----- 653
Db 3771 AAGATCCGGAAGTACAGATGCGGAGACTGCTGCAGGAAACGGAGCTGTGGAGCCGCTG 3830
QY 653 ----- 653
Db 3831 ACACCTAGCGGAGCGATGCCAACACGAGCGCAGATGGGATCCTGAAAGAGACGGAGCTG 3890
QY 653 ----- 653
Db 3891 AGGAAGTGAAGTGTCTGGATCTGGCGCTTTTGGCACAGTCTCAAGGGGCATCTGGATC 3950
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Db 3951 CCTGATGGGGAGAAATGAAATTCAGTGGCCATCAAAAGTTGTGAGGGAACACATCC 4010
QY 653 ----- 653
Db 4011 CCCAAGGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGCTGGTGGGCTCCCCA 4070
QY 653 ----- 653
Db 4071 TATGTCTCCCGCTCTCTGGGCATCTGCTGACATCCACGGTGCAGCTGTGTGACACAGCTT 4130
QY 653 ----- 653
Db 4131 ATGCCCTATGGCTGCTCTTAGACCATGTTCGGGAAACCGGGAACCGCTGGGCTCCGAG 4190
QY 653 ----- 653
Db 4191 GACCTGCTGAACTGGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4250
QY 653 ----- 653
Db 4251 CTGCTACACAGGACTTGGCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 4310
QY 653 ----- 653
Db 4311 ATTACAGACTTCGGGTGGCTCGGCTGCTGGAATTTGAACAGACAGATACCATGAGAT 4370
QY 653 ----- 653
Db 4371 GGGGGCAAGGTGCCCATCAAGTGGATGGCGTGGAGTCCATTTCTCCCGCGGCTTCACC 4430
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RESULT 13

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Db 4431 CACCAGAGTGAATGTGTGGAGTTATGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 4490
QY 653 ----- 653
Db 4491 AAACCTTACGNTGGATCCAGCCCGGAGATCCCTGACCTGCTGGAAAAGGGGAGCGG 4550
QY 653 ----- 653
Db 4551 CTGCCCCAGCCCCCATCTGCAACATTGATGTCTACATGATCATGTTGGTCAAAATGTTGATG 4610
QY 653 ----- 653
Db 4611 ATTGACTCTGAATGTGCGCCCAAGATTCCGGAGTGTGTTCTGTAATTTCTCCCGATGGCC 4670
QY 654 ----- 664
Db 4671 AGGACCCCGCGCTTTTGTGTCATCCAGATGAGGACTTTGGCCCCAGCCAGTCCCTTG 4730
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 4731 GACAGCACCTTTCTACCGCTCACTGCTGAGGACGATGACATGAGGACCTGGGCTGGTGGT 4790
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 4791 GAGGAGTATCTGTATCCCAAGCAGGCGCTTCTCTGTCAGACCTGCCCCGGGCGCTGG 4850
QY 705 GlyMetValHisIleArgHisArgSerSerThrArgSerGlyGlyValAspLeuThr 724
Db 4851 GGATGCTCCACACAGGACCCGAGCTCATCTACAGGAGTGGCGGTGGGAGACTGACA 4910
QY 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 4911 CTAGGCTGGAGCCCTCTGAAGAGGAGGCCCCCGAGTCTCCACTGGCACCTCCGAGG 4970
QY 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
Db 4971 GCTGGCTCCGATGATATTTGATGTTGACCTGGGAATGGGGGCGAGCAAGGGCTTCAAG 5030
QY 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 5031 CTCCACACATGACCCCGAGCTCTACAGCGGTACAGTGGAGGCCCCACAGTACCTCC 5090
QY 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 5091 CCTCTGAGACTGATGCTAGCTTGGCCCCCTGACCTGACGCCCCAGCCCTGATATGTG 5150
QY 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 5151 AACGAGCCAGATGTTGGGCCCGAGCCCTTTCGCCCGAGAGGGGCTCTGCTGCTGCTGCC 5210
QY 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 5211 CGACCTGCTGTGTCCTCTGGAAGGGGCCAGACTCTCTCCCGAGGAGAGATGGGGTC 5270
QY 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 5271 GTCAAAGACGTTTTTGGCTTTGGGGTGGCTGGAGAACCCCGAGTACTTTGACACCCAG 5330
QY 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 5331 GGAGGAGCTGCCCTCAGGCCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5390
QY 885 TyrTyrTyrAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 5391 TATTACTGGGACCAAGACCCACAGAGCGGGGGCTTCCACCCAGCACCTTCAAGAGGACA 5450
QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 5451 CCTACGGCAGAGAACCCAGAGTACTGGGTCTGGAGCTGGAGCTGCGCAGTG 5495
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QY 823 AlaAlaArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsn 842
 DB 3506 CCTGTCCGGCCCTGCTGGTGCTACTCTAGAAAGACCCAGACTCTCTCTCTGGGAGGAAAT 3565
 QY 843 GlyValValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluThrLeuThr 862
 DB 3566 GGGGTGTCAAGACGTTTGGCTTGGGGGTGCTGTGGAGAACCTTGATACCTTAGTA 3625
 QY 863 ProGlnGlyGlyAlaAlaProGlnProHisProProProProAlaPheSerProHisPheAsp 882
 DB 3626 CCGAGAGAAGGCACTGCTCTCCGCCCCACACCTTCTCTGCTTCCAGCCCAAGCTTTGAC 3685
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 DB 3686 AACCTCTATTACTGGGACCAAGACTCATCGGAGCGAGGGCCCTCCACCAAGTAACCTTTGAA 3745
 QY 903 GlyThrProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
 DB 3746 GGGACCCCACTGCAGAGAACCTTGATAGCTAGGCTGGATGACTCTGTA 3796

RESULT 15

US-09-146-283-3
 : Sequence 3, Application US/09146283
 : Patent No. 5976546
 : GENERAL INFORMATION:
 : APPLICANT: Laus, Reiner
 : APPLICANT: Wu, Hongyu
 : TITLE OF INVENTION: Immunostimulatory Compositions
 : NUMBER OF SEQUENCES: 10
 : CORRESPONDENCE ADDRESS:
 : ADDRESSES: Dehlinger & Associates
 : STREET: 350 Cambridge Ave. Suite 250
 : CITY: Palo Alto
 : STATE: CA
 : COUNTRY: USA
 : ZIP: 94306
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/146,283
 : FILING DATE: 03-SEPT-1998
 : CLASSIFICATION: 536
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Judge, Linda R.
 : REGISTRATION NUMBER: 42,702
 : REFERENCE/DOCKET NUMBER: 7636-0010.21
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 650-324-0880
 : TELEFAX: 650-324-0960
 : INFORMATION FOR SEQ ID NO: 3:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 2385 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: double
 : TOPOLOGY: linear
 : MOLECULE TYPE: DNA (genomic)
 : HYPOTHETICAL: NO
 : ANTI-SENSE: NO
 : ORIGINAL SOURCE:
 : ORGANISM: homo sapiens
 : INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig. 8
 : US-09-146-283-3

Alignment Scores:

Pred. No.: 6,91e-261 Length: 2385
 Score: 3632.00 Matches: 659
 Percent Similarity: 98.65% Conservative: 0
 Best Local Similarity: 98.65% Mismatches: 5

Query Match: 71.52% Indels: 4
 DB: 2 Gaps: 2
 US-09-493-480-6 (1-919) x US-09-146-283-3 (1-2385)
 QY 1 MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProProGlyAla 20
 DB 11 ATGGAGCTGGGGCCCTTGTGGCGCTGGGGGCTCTCTCGCCCTCTTGTGCCCCCGAGCC 70
 QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
 DB 71 GCGAGACCCCAAGTGTGACCCGACAGCATGAAGCTGGGCTCTCTGCCAGTCCCGAG 130
 QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
 DB 131 ACCCACTGGACATGCTCGCCCACTCTACCAAGGCTGCCAGGTGTGTGAGGAAACCTG 190
 QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
 DB 191 GAACTCACCTACCTGCCCAATGCCAGCTGTCTTCTGCGAGGATATCCAGGAGGTG 250
 QY 81 GlnGlyTyrValLeuIleAlaHisGlnGlnValArgGlnValProLeuGlnArgLeuArg 100
 DB 251 CAGGGCTAGTGCTCATGCTCTCAACCAAGTGAGGAGGTCCCACTGCGAGGCTGCGG 310
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 DB 311 ATTGTGGAGGACCCAGCTCTTTGAGGACAATATGCTTGGCGCTGTGTAGACAAATGA 370
 QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
 DB 371 GACCCGCTGAACAATACCACTGTGTACAGGGGCTTCCCAAGAGGAGGCTTGGCGGAGCTG 430
 QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
 DB 431 CAGCTTTCGAAGCTCTACAGAGATCTTGAAGAGGGGGTCTTGTATCCAGCGGAAACCCCG 490
 QY 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnGlnLeuAla 180
 DB 491 CTCTGTACCAAGGACACGATTTGTGGAAGGACATCTTCCACAAGAACAACCACTGGCT 550
 QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
 DB 551 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCGCCCTGTTCTCGATGTGTAA 610
 QY 201 GlySerArgCysThrGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
 DB 611 GGCTCCCGCTGCTGGGGAGAGAGTCTTGAGGATTGTGAGAGCTTGAGCCGCACTGTCTGT 670
 QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
 DB 671 GCCGGTGGCTGTGCGCTGCAAGGGGCCACTGCCCACTGACTGTGCTGCAATGAGCAGTGT 730
 QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
 DB 731 GCTGCGGGCTGCACGGGGCCCCCAAGCACTCTGACTGTGCTGGCGCTGCCCTTCAACCA 790
 QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
 DB 791 AGTGGCATCTGTGAGGCTGCACTGCCCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 850
 QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
 DB 851 TCCATGCCCAATCCCGAGGGCCGGTATATACATTGGGGCCAGCTGTGTGAGCTGCTGCTG 910
 QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
 DB 911 TACAACCTTACCTTTCTAGGAGCGTGGGATCTCTGCACTTGTGAGAGTGTGAGAGTGTGAG 970
 QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
 DB 971 GAGGTGACACAGAGAGTGGNACACAGCGGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 1030

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QY 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
DB 1031 GTGTGCTATATGCTGGGCTATGGAGCACTTCGGAGAGGTGAGGGGAGTTACCACTGCCAAT 1090
QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
DB 1091 ATCCAGAGATTGCTGGCTGCAAGAGATCTTTGGGAGCCTGGCAATTTCTGCCGGAGAGC 1150
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
DB 1151 TTTGATGGGAGCCAGCCTCCAACACTCCCGCTCCAGCCAGAGCAGCTCCAAGTGT 1210
QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
DB 1211 GAGACTCTGGAAGAGATCAAGGTTACCTATATCTCAGCATGGCCGGACAGCTGCCT 1270
QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
DB 1271 GACCTCAGCGTCTTCCAGAACCTGCAAGTAAATCCGGGACGAAATTCGCACAAATGGGCC 1330
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
DB 1331 TACTCGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGCGTCACTGAGGGAA 1390
QY 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
DB 1391 CTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCACCTCTGCTTCGTCACACGGTG 1450
QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
DB 1451 CCTGGGACCGAGTCTTTCCGAAACCCGACCAAGCTCTGCTCCACACTGCACACCGGCCA 1510
QY 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
DB 1511 GAGGACGAGTGTGTGGGCGAGGGCTGGGCTGCGCCAGCTGTGCGCCCGAGGGCACTGC 1570
QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
DB 1571 TGGGGTCCAGGGGCCACCCAGTGTGTCACTGCAGCCAGTTCTCTTCGGGGCCAGGAGTGC 1630
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
DB 1631 GTGGAGGAATGCCGAGTACTGCGGGGCTCCCGAGGGAGTATGTGAATGCCAGGCACTGT 1690
QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
DB 1691 TTGCCGTGCCACCTGAGTGTGAGCCAGAAATGGCTCAGTGACCTGTTTGGACCGGAG 1750
QY 581 AlaAspGlnCysValAlaCysAlaHisTyrIysAspProPheCysValAlaArgCys 600
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GenCore version 5.1.6
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Run on: June 7, 2004, 13:54:19 ; Search time 830.537 Seconds

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Title: US-09-493-480-6

Perfect score: 5078

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2995936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters: 5991872

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	4900	96.5	3768	13	US-09-765-973-1	Sequence 1, Appli
4	4900	96.5	3768	15	US-10-313-644-1	Sequence 5, Appli
5	4900	96.5	4473	10	US-09-441-411-5	Sequence 32, Appli
6	4900	96.5	4473	15	US-10-146-473-32	Sequence 44, Appli
7	4900	96.5	4473	15	US-10-207-655-44	Sequence 81, Appli
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11	4892	96.3	3768	9	US-09-811-115-2	Sequence 3, Appli
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23	4892	96.3	4530	16	US-10-117-937-595	Sequence 208, App
24	4892	96.3	4530	16	US-10-159-563-208	Sequence 10, Appli
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33	4134	81.4	3955	10	US-09-751-708A-117	Sequence 117, App
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ALIGNMENTS

RESULT 1

US-09-854-356-9
; Sequence 9, Application US/09854356
; Patent NO. US20020177567A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Gheysen, Dirk
; APPLICANT: Corixa Corporation
; APPLICANT: SmithKline Beecham Biologicals S. A.
; TITLE OF INVENTION: HER-2/neu Fusion Proteins
; FILE REFERENCE: 014058-009810PC
; CURRENT APPLICATION NUMBER: US/09/854,356
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 09/493,480
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,976
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens

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; Sequence 1, Application US/09930125
; Publication No. US20020193329A1
; GENERAL INFORMATION:
; APPLICANT: Hand-Zimmerman, Susan
; APPLICANT: Cheever, Martin A.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.

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3121 GGCATGCTCCACCAAGGCAACCGAGCTCATCTACAGGAGTGGCGGTGGGACCTTGACA 3180
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3601 GGAGGAGTGGCGCTTCCAGCCCGAGCGGCGGCTCTCTGCTCTTCCAGCCAGCTTTCGACAACTC 3660
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RESULT 3

US-09-765-973-1

; Sequence 1, Application US/09765973

; Publication No. US20020039573A1

; GENERAL INFORMATION:

; APPLICANT: Cheever, Martin A.

; APPLICANT: Hand-Zimmermann, Susan

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR PREVENTION AND

; TITLE OF INVENTION: TREATMENT OF HER-2/neu ASSOCIATED MALIGNANCIES

; FILE REFERENCE: 210121.496

; CURRENT APPLICATION NUMBER: US/09/765,973

; CURRENT FILING DATE: 2001-01-19

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 3768

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1) ... (3765)

US-09-765-973-1

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Score: 4900.00

Length: 3768

Matches: 919

Conservative: 0

Percent Similarity: 73.23%

Best Local Similarity: 73.23%

Mismatch: 0

Query Match: 96.49%

Indels: 336

Gaps: 1

DB:

US-09-493-480-6 (1-919) x US-09-765-973-1 (1-3768)

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DB 61 GCGAGCACCAAGTGTGACGCGGACAGACATGAAGCTGCGGCTCCCTGCGAGTCCGAG 120
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QY 61 GluLeuThrTyrrLeuProThrAnalaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
DB 181 GAACCTACCTACTGCTGCCACCAATGCGAGCTGTCTTCTGCGAGTATCCAGAGGTG 240
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QY 121 AspProLeuAsnAnthrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
DB 361 GACCCGCTGAACATACCAACCCCTGTACAGGGGCTCCCGAGAGGCTGCGGAGCTG 420
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln 160
DB 421 CAGCTTCGAAGCCTCAGAGATCTTGAAGAGGAGGCTCTTGTATCCAGCGGAAACCCCGAG 480
QY 161 LeuCysTyrrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAnGlnLeuAla 180
DB 481 CTCTGCTACAGAGACAGATTTGTGAAGAGACATCTTCCACAGAAACACCAAGCTGGCT 540
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QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
DB 721 GCTGCGGCTGCGAGGCGGCCCAAGCACTCTGACTGCTGCGCTGCTCCACTTCAACCA 780
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrrAnthrAspThrPheGlu 280
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DB 781 ACTGGCATCTGGAGCTGCACTGCCCGCCCTGGTCACTTACCAACAGACACGTTTGAG 840
QY 281 SerMetProAsnProGluGlyArgTyrrPheGlyAlaSerCysValThrAlaCysPro 300
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QY 301 TyrrAsnTyrrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
DB 901 TACAACCTACTCTTCTACGGAGCGTGGATCTGACACCTCTGCTGCGCCCTGCAACACNA 960
QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
DB 961 GAGGTGACAGCAGAGATGGAACACAGCGGTGTGAGAGTGTGAGAGGCTTGTGCCCGGA 1020
QY 341 ValCysTyrrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
DB 1021 GTGTGCTATGCTTGGGCTGAGGACATTTGCGAGAGTGTGAGGCGAGTTACCACTGCTCA 1080
QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
DB 1081 ATCCAGGAGTTTGTGCTGCAAGAAAGATCTTTGGGAGCTTGGCATTTCTGCGGAGAGC 1140
QY 381 PheAspGlyAspProAlaSerAnthrAlaProLeuGlnProGluGlnValPhe 400
DB 1141 TTTGATGGGAGCCAGCTTCCAACTGCCCCCTCCAGCCAGAGAGCTTCCAAGTGT 1200
QY 401 GluThrLeuGluGluIleThrGlyTyrrLeuTyrrIleSerAlaTrpProAspSerLeuPro 420
DB 1201 GAGACTCTGGAAGAGATCACAGGTATCTTACCTATATATCTCAGCATGCGCGAGAGCTGCCT 1260
QY 421 AspLeuSerValPheGlnAnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
DB 1261 GACCTCAGGCTCTTCCAGAACCTGCAAGTAATCCGGGAGCAATTTCTGCACAAATGGCGCC 1320
QY 441 TyrrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
DB 1321 TACTCTGCTGACCTGCAAGGCTGGGCTCAGCTGGCTGGGCTGCGCTCTCTCTGAGGGA 1380
QY 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
DB 1381 CTGGGAGTGGAGTGGCCCTCATCCACATAACACCCACTCTGCTGCTGTCGACACAGGTG 1440
QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
DB 1441 CCCTGGGAGCAGCTCTTTCGAAACCCGACACCAAGCTCTGCTCCACACTGCAACCGGCA 1500
QY 501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
DB 1501 GAGGACAGTGTGTGGGCGAGGCGCTGGCTGCCACCAAGCTGTGCGGCCGAGGAGTGC 1560
QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
DB 1561 TGGGCTCCAGGCGCCACCCAGTGTGTCACTGAGCCAGTCTCTTCTGGGCGCAGAGTGC 1620
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrrValAnalaArgHisCys 560
DB 1621 GTGGAGGAATGCGGAGTACTGCGAGGCTCCCGAGGAGTGTGGAATGCGCAGGAGTGT 1680
QY 561 LeuProCysHisProGluCysGlnProGlnAnGlySerValThrCysPheGlyProGlu 580
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QY 601 ProSerGlyValLysProAspLeuSerTyrrMetProIleTrpLysPheProAspGluGlu 620
DB 1801 CCCAGCGGTGAAACCTGACCTCTCTATATGCCCCATCTGGAAGTTCCTCAGATGAGGAG 1860
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Db 2461 GACCTGCTGAATGGTGTATGCAGATTGCCAAGGATGAGTACCTGGAGGATGTGCGG 2520
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Db 2521 CTCGTACACAGGACTTGGCGCTCGGAACGTGCTGTGTCAGAGTCCAAACCATGTCAAA 2580
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Db 2581 ATTACAGACTTGGGCTGGCTGGCTGCTGGAATTGACGAGACAGTACCATGCAGAT 2640
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Db 2761 AAACCTTACGATGGATCCCGCGCGGAGATCCCTGACCTGTGTGGAAGGGGGAGCGG 2820
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Db 2821 CTGCCCCAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGTGTCAAAATGTTGATG 2880
Qy 653 ----- 653
Db 2881 ATTGACTCTGAATGTCCGCCAAGATTCGGGAGTGTGTGTCTGAAATTTCTCCCGCATGGCC 2940
Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGACCCCCAGCGCTTTGTGTGTCATCCAGAAATGAGGACTTGGCCCGCAGTCCCTTG 3000
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Qy 665 AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGCACCTTCTTACCGCTCACTCTGTGAGGACGATGACATGGGGGACCTGTGTGATGCT 3060
Qy 685 GluGluTyrLeuValProGlnGlnGlyPheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGATATCTGTGTATCCCGACGAGGGCTTCTTGTTCAGACCTCTGCCCCGGGCGCTGG 3120
Qy 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
Db 3121 GGCATGCTCCACACACAGCCAGCTCATCTACAGGAGTGGCGTGGGACCTGACA 3180
Qy 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGlyGly 744
Db 3181 CTAGGGCTGGAGCCCTCTGAAGAGAGGCGCCCGAGGTCTTCCACTGGCACCTTCGAAGGG 3240
Qy 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
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Qy 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3361 CCCTCTGAGACTGATGCTAGTGTGCCCCCTGACCTGCAGCCCCCAGCCTGGAATATGTG 3420
Qy 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3421 AACGACGAGATGTTGGCCCCAGCCCCCTTTCGCCCGAGAGGGCCCTCTGCTGCTGCC 3480
Qy 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3481 CGACCTGCTGGTCCACTCTCTGGAAGGCCCAAGACTCTCTCCCCAGGCAAGAAATGGGTC 3540
Qy 845 ValIysAspValPheAlaPheGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3541 GTCAAGACGCTTTTGTGCTTGGGGGTGCCGTGGAGAACCCCGAGTACTTGCACCCCCAG 3600
Qy 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3601 GGAGGAGCTGCCCTCTAGCCCCACCTCTCTCTGCTTCCAGCCAGCCTTTCAGACACCTC 3660
Qy 885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3661 TATTACTGGGACAGGACCCACAGAGCGGGGGCTCCACCAGCACCTTCAAGGGGACA 3720
Qy 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3721 CCTACGGCAGAGAACCCAGAGTACTTGGGTCTGGACGTCGCCAGTG 3765
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RESULT 4

US-10-313-644-1

; Sequence 1, Application US/10313644

; Publication No. US20030157119A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Cheever, Martin A.

; APPLICANT: Hand-Zimmerman, Susan

; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL

; TITLE OF INVENTION: AND VIRUS-ASSOCIATED MALIGNANCIES

; FILE REFERENCE: 210121.483C3

; CURRENT APPLICATION NUMBER: US/10/313,644

; CURRENT FILING DATE: 2002-12-04

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 3768

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: CDS
; LOCATION: (1)....(3765)
US-10-313-644-1

Alignment Scores:

Pred. No.: 0 Length: 3768
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 15 Gaps: 1

US-09-493-480-6 (1-919) x US-10-313-644-1 (1-3768)

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Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 61 GCGAGCACCAAGTGTGACCGGGCAGACATGAAGCTGGGGCTCCCTGCCAGTCCCGAG 120
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTrpGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 121 ACCACCTGGACATCTCCGCCACTCTTACAGGGCTGCCAGTGGTGGAGGAAACCTG 180
Qy 61 GluLeuThrTrpLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
Db 181 GAACCTCACTACCTGCCCAACCAAGTGGAGGAGGTCCCACTGCAGATATCCAGGAGTG 240
Qy 81 GlnGlyTrpValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
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Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTrpAlaLeuAlaValLeuAspAsnGly 120
Db 301 ATTGTGCGAGGCCAGCTCTTTGAGGACACTATGCTCCCTGGCTGTGTAGACATGGA 360
Qy 121 AspProLeuAsnAsnThrTrpValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 361 GACCCGCTGAACAAATACCACTCTGTACAGGGGCTCCCAAGGAGGCTGGCGGAGCTG 420
Qy 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 421 CAGCTTCGAAGCTCACAGAGATCTTGAAGGAGGGGTCTTGATCCAGCGGAACCCCGAG 480
Qy 161 LeuCysTrpGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 481 CTCTGCTACCGAGACACGATTTTGGAGGAGACACTTCCACAGACACACAGCTGGCT 540
Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 541 CTCACATGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTTCTCCGATGTGTAG 600
Qy 201 GlySerArgCysTrpGlyLeuSerSerGluAspCysGlnSerLeuThrArgTrpValCys 220
Db 601 GGCCTCCGCTGTGGGAGAGAGTCTTGAGGATGTGACAGCTTGACGGCGCACTGTCTGT 660
Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
Db 661 GCGGGTGGTGTGGCGCTGCAAGGGGCCACTGCCCACTGACTGTGCTGCCATGAGCAGTGT 720
Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
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Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTrpAsnThrAspThrPheGlu 280
Db 781 AGTGGCATCTGTGAGCTGACCTGCCCGCCCTGGTCACTTACCAACAGACACAGCTTGG 840
Qy 281 SerMetProAsnProGluGlyArgTrpThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 841 TCCATGCCCCCAATCCCGAGGGCCGGTATATCATTTGGGGCCAGCTGTGTGACTGCTGCC 900

Qy 301 TyrAsnTrpLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db 901 TACAACCTACCTTTCTACGGACGTGGATCTCTCACCCCTCTGCCCCCTTGCACAACCAA 960
Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
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Db 1021 GTGTCTATGGTCTGGGCATGGAGCACTTGCAGAGGTGAGGCGAGTTACAGTGCCTAAT 1080
Qy 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 1081 ATCCAGAGTTTGTCTGGCTGCAAGAGATCTTTGGAGGCTTGCCATTTCTGCCGAGAGC 1140
Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
Db 1141 TTTGATGGGACCCAGCTCCAACTGCCCGCTCCAGCCAGAGCAGCTCCAAGTGTGT 1200
Qy 401 GluThrLeuGluGluIleThrGlyTrpLeuTrpIleSerAlaTrpProAspSerLeuPro 420
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Db 1261 GACCTCAGCGCTTCCAGAACCTGCAAGTAATCCGGGGACGAATTTCTGCAATGGCGCC 1320
Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
Db 1321 TACTCGCTGACCTGCAGGGCTGGGCATCAGCTGGCTGGGGCTGGCTCCTCCTGAGGAA 1380
Qy 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
Db 1381 CTGGGCGAGTGAGCTGGCCCTCATCCACCAACACACCTCTGCTCTGCTGTCACAGGTG 1440
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Db 1441 CCTCGGACCACTCTTTCGGAACCCGACCAAGCTCTGCTCCACTGCTCCACACCGGCCA 1500
Qy 501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
Db 1501 GAGGACGAGTGTGTGGCGAGGGCTGGCTGCCACCACTGTCGCCCGCGAGGCACTGC 1560
Qy 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Db 1561 TGGGGTCCAGGGCCCAACCCAGTGTGTCAACTGCAGCCAGTTCTTCCGGGCCAGGAGTGC 1620
Qy 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTrpValAsnAlaArgHisCys 560
Db 1621 GTGGAGGAATGCCGAGTACTGCAAGGGGCTCCCGAGGAGTATGTGATGTCAGGCACTGT 1680
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Qy 581 AlaAspGlnCysValAlaCysAlaHisTrpLysAspProPheCysValAlaArgCys 600
Db 1741 GCTGACAGTGTGGCCCTGTGCCCCTATAGGACCTCCCTCTCTGCGGGCCCGCTGC 1800
Qy 601 ProSerGlyValLysProAspLeuSerTrpMetProIleTrpLysPheProAspGluGlu 620
Db 1801 CCAGCGGTGTGAACCTGACCTCTCTACATGCCCATCTGGAGTTCCTCAGATGAGGAG 1860
Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
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Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
Db 1921 GGTGCCCCCGGAGCAGAGAGCCCTCTGACGTCCATCATCTCTCGGTGGTGGTGGC 1980

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Db 1981 ATTCTGCTGTCGTGCTTTGGGGTGTCTTTGGGATCTCTCATCAAGCCGACGACGAG 2040
QY 653 ----- 653
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QY 653 ----- 653
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Db 3121 GGCATGTTCCACACACGCGACGCTCATCTACAGAGTGGCGGTGGGACCTGACA 3180
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QY AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaGlyGlyLeuGlnSer 764
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Db 3661 TATTACTGGGACGAGGCCACGAGCGGGGGCTCCACCCAGCACCTTCAAGGGACA 3720
QY ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3721 CCTACGGCAGAGAACCACGAGTACTGCTGGTCTGGAGCTGCCAGTG 3765

RESULT 5

US-09-441-411-5
; Sequence 5, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Inggerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-441-411-5

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0

Query Match:	96.49%	Indels:	336
DB:	10	Gaps:	1
US-09-493-480-6 (1-919) x US-09-441-411-5 (1-4473)			
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QY	21	AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu	40
DB	235	GGAGGACCCCAAGTGTGACCGGCACAGCATGAGCTGGGCTCTCTGCGAGTCCCGAG	294
QY	41	ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu	60
DB	295	ACCCACCTGGACATGCTCGCCACCTCTACAGGGCTGCAGGTGGTGCAGGGAACCTG	354
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DB	355	GAACCTCACCTACCTGCCCCACCAATGCCAGCTGTCTCTCTGCGAGATATCCAGGAGGTG	414
QY	81	GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100
DB	415	CAGGGCTAGTGTCTCATCTCTACCAACCAAGTGAGGACAGTCCCACTGCAGAGCTGCGG	474
QY	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120
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QY	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140
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QY	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln	160
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QY	161	LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla	180
DB	655	CTCTGTACAGGACACCATTTGTGGAAGGACATCTTCCACAAGAACCAACCAAGCTGGCT	714
QY	181	LeuThrLeuLeuAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
DB	715	CTCACACTGATAGACCAACCGCTCTCGGGCTTGCACCCCTGTCTCCGATGTGTAA	774
QY	201	GlySerArgCysTrpGlyGluSerSerGlnAspCysGlnSerLeuThrArgThrValCys	220
DB	775	GGCTCCCGCTGTGGGGAGAGTCTTGAGGATGTTCAGAGCTTGACGGCGCACTGTCTGT	834
QY	221	AlaGlyGlyCysAlaAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	240
DB	835	GCCGGTGGCTGTGCCCGCTGCAAGGGGCCACTGCCCACTGACTGTGCTGCCATGAGCAGTGT	894
QY	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
DB	895	GCTGCCGGCTGCAAGGGGCCCAAGCACTCTGACTGTGCTGGCTGCTCTCACTTCAACCA	954
QY	261	SerGlyLeuCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280
DB	955	AGTGGCATCTGTGAGCTGCACTGCCCGGCTGTGCTCACCTACCAACACAGACAGTGTGAG	1014
QY	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300
DB	1015	TCCATGCCCAATCCCGAGGGCCGGTATACATTCGGCGCCAGCTGTGTGCTGTCTGTCCC	1074
QY	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
DB	1075	TACAACTACTTTCTACGGACGTGGGATCTCTGACCCCTGTGCTGCTGCTGCAACACCA	1134
QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340
DB	1135	GAGGTGACAGCAGAGGATGGAACACAGACCGGTGTGAGAGTGCAGAGCGCTGTGCCCCA	1194
QY	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
DB	1195	GTGTGCTATGGTCTGGGCATGGAGCACTTTCGAGAGGTGAGGCGAGTTACGAGTGCCAAT	1254
QY	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380
DB	1255	ATCCAGAGTGTGTGGCTGCAAGAGATCTTTGGGAGCTTGGCATTTCTGCCGAGAGC	1314
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400
DB	1315	TTTGATGGGACCCAGCTCCCAACACTGCCCCGCTCCAGCAGAGCAGCTCCAAGTGTGT	1374
QY	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	420
DB	1375	GAGACTCTGGAAGAGATCAAGTTACTATATCATCTCAGCATGGCGGACAGCGCTGCGCT	1434
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyValGileLeuHisAsnGlyAla	440
DB	1435	GACCTCAGGCTCTTCGGAACCTGCAAGTANTCCGGGACGANTTTCGCACATATGGCGCC	1494
QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
DB	1495	TACTGCTGACCTGCAGGGCTGGGCATCAGCTGCTGGGCTGGCGCTCCTCAGTGAGGAA	1554
QY	461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480
DB	1555	CTGGGAGTGAGCTGGCCCTCATCCACCATTAACCCACCTCTGCTGTGTGTCACACCGTG	1614
QY	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
DB	1615	CCCTGGGACCACTCTTCGGGAACCCGACCAAGCTCTGCTCCACACTGCTCCACCGGCCA	1674
QY	501	GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
DB	1675	GAGGACAGTGTGTGGCGGAGGCTGGGCTGTCACAGCTGTGGCGCCGAGGGCACTGC	1734
QY	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
DB	1735	TGGGGTCCAGGGGCCACCCAGTGTGTCAACTGCGAGCAGTGTCTTCCGGGCCAGGAGTGC	1794
QY	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560
DB	1795	GTGGAGGATGCGAGTACTGCGAGGGGCTCCCGAGGGAGTATGTGAATGCGAGCACTGT	1854
QY	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
DB	1855	TTGCGCTGGCCACCTCAGTGTTCAGCCCGAGATGGCTCAGTGACCTGTTTTTGACCGGAG	1914
QY	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys	600
DB	1915	GCTGACAGTGTGTGGCTGTGCCCACTATAGGACCTCTCCCTTCTGCGTGGCGCGCTGC	1974
QY	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu	620
DB	1975	CCCGGGGTGGAACCTGACCTCTCTCATGCCCATCTGGAAGTTTCAGATGAGAG	2034
QY	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640
DB	2035	GGCGCATGCGAGCTTTGCCCATCAACTGACCCACTCTCTGTTGTGGACCTGGATGACAG	2094
QY	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
DB	2095	GGTGGCCCCCGGACGAGAGGACGAGCCCTCTGACGCTCATCTCTGCGGTGGTGGC	2154
QY	653	-----	653
DB	2155	ATTCTGCTGCTGCTGCTTGGGGTGTCTTTGGATCTCTCATCAAGCGACGAGCAG	2214
QY	653	-----	653
DB	2215	AAGATCCGGAAGTACACGATGCGGAGACTGCTGACGAGAAACGGAGCTGGTGGAGCGCTG	2274
QY	653	-----	653

Db 2275 ACACCTAGCGGAGCGATGCCCAACCAAGCGCAGATCGGATCTCTGAAGAGACGAGCTG 2334
QY 653 ----- 653
Db 2335 AGGAAGGTGAGGTGCTTGATCTGGCGCTTTTGGCACAGCTCTACAAGGGCACTGGATC 2394
QY 653 ----- 653
Db 2395 CCTGATGGGAGAATGTGAAAAATTCAGTGGCCATCAAGTGTTCAGGGAACACACATCC 2454
QY 653 ----- 653
Db 2455 CCCAAGCCAAAGAAATCTTAGACGAAGCATACGTGATGCTGCTGGGCTCCCA 2514
QY 653 ----- 653
Db 2515 TATGTCTCCGCTCTTCGGGCATCTGCTGACATCCAGGTGCAGCTGGTGACACAGCTT 2574
QY 653 ----- 653
Db 2575 ATGCCCTATGCTGCTCTCTTAGACCAATGTCGGGAAACCGCGACGCTGGGCTCCAG 2634
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Db 2635 GACCTGCTGAACCTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2694
QY 653 ----- 653
Db 2695 CTGTTACACAGGACTTTGGCGCTCGGACGCTGCTGCTCAAGAGTCCCAACCATGTCAAA 2754
QY 653 ----- 653
Db 2755 ATTACAGACTTCGGGCTGGCTCGCTGCTGCACATTCAGCAGACAGAGTACCATGCAGAT 2814
QY 653 ----- 653
Db 2815 GGGGCAAGGTGCCATCAAGTGAATGGCGCTGAGTCCATTCTCCCGCGCGGTTCAAC 2874
QY 653 ----- 653
Db 2875 CACCAGATGATGTGGAGTTATGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2934
QY 653 ----- 653
Db 2935 AAACCTTAACGATGGATCCAGCCCGGAGATCCCTGACCTGTGGAAGAGGGGAGCGG 2994
QY 653 ----- 653
Db 2995 CTGCCCCAGCCCCCATCTGCACCCATTTGATGTCTACATGATCATGTGTCAAATGTTGGATG 3054
QY 653 ----- 653
Db 3055 ATTGACTCTGAATGTCCGCCAAGATTCGGGAGTTGTGTCTGTAATTTCTCCGCATGGCC 3114
QY 654 ----- GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3115 AGGGACCCCGCGCTTTGTGTCTATCCAGATGAGGACTTGGCCCGCAGCAGTCCCTTG 3174
QY 665 AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3175 GACAGCACCTTTCTACCGCTCACTGCTGGAGGACATGACATGGGGGACCTGGTGGATGCT 3234
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyValaGly 704
Db 3235 GAGGAGTATCTGTGTACCCAGAGGGCTTCTTGTCCAGACCTTCGCCCGCGGCTGGG 3294
QY 705 GlyMetValHisHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
Db 3295 GGATGTTCCACACAGCACCGCAGCTCATCTACAGGAGTGGCGGTGGGACCTGCACA 3354
QY 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744

Db 3355 CTAGGCTGGAGCCCTCTCTGAGAGGAGCGCCCGAGGTCTCCACTGGCACCCCTCCGAAGGG 3414
QY 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
Db 3415 GCTGGCTCCGATGTAATTTGATGTGTGACTGCTGGATGGGGCAGCCAGGGGCTGCAAGC 3474
QY 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 3475 CTCCCCACATGATACCCAGCCCTCTACAGGGGTACAGTGAAGGACCCACAGTATCCCTG 3534
QY 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3535 CCTCTGAGACTGATGTGCTAGTTCCTCCCTGACTGACCTGCAGCCCCCAGCCTGATATGTG 3594
QY 805 AsnGlnProAspValArgProGlnProSerProArgGluGlyProLeuProAlaAla 824
Db 3595 AACCCAGCAGATGTTGGGCCCGCCAGCCCTCTCGCCCGAGAGGGCCCTCTGCTGCTGCC 3654
QY 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3655 CGACCTGCTGGTGCCTCTGGAAGGCCCAAGACTCTCTCTCCCGAGGGAAGTGGGTCT 3714
QY 845 ValLysAspValPheAlaPheGlyValAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3715 GTCAAGACGTTTTTGGCTTTGGGGGTGCGCTGGAGAACCCCGAGTACTTGACACCCCG 3774
QY 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3775 GGAGGAGTCCCTCAGCCCGCCCTCTCTCTGCTTCCAGCCCGCAGCTTCGACAACTC 3834
QY 885 TyrTyrTrpAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3835 TATTACTGGGACCAAGGACCCACCAAGAGGGGGGCTCCACCCAGCACCTTCAAGAGGACA 3894
QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3895 CCTACGCGCAGAGAACCCAGAGTACTGCGTCTGACAGTGCACGTGCCAGTG 3939

RESULT 6

US-10-146-473-32
; Sequence 32, Application US/10146473
; Publication No. US2003010888A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tseeng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146,473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-473-32

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 15 Gaps: 1

US-09-493-480-6 (1-919) x US-10-146-473-32 (1-4473)


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Db 2335 AGGAAGTGAAGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAGGGCATCTGGATC 2394
Qy 653 ----- 653
Db 2395 CCTGATGGGAGAAATGTGAAATTCAGTGGCCATCAAAGTGTGAGGAAAAACACATCC 2454
Qy 653 ----- 653
Db 2455 CCCAAAGCCAAAGAAATCTTAGACGAAGCATAOGTGAATGGCTGGGTGCCCA 2514
Qy 653 ----- 653
Db 2515 TATGTCCTCCGCTTCTGGGCATCTGCTGACATCCAGGTGCAGCTGGTGACACAGCTT 2574
Qy 653 ----- 653
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Qy 653 ----- 653
Db 2635 GACCTGCTGAATCGTGTATGACATTTGCCAAGGGGATGAGCTACCTGGAAGATGTGCGG 2694
Qy 653 ----- 653
Db 2695 CTGCTACACAGGACTTTGGCCGCTCGGAACTGTCTGTGTCAGAGTCCCAACCATGTCAA 2754
Qy 653 ----- 653
Db 2755 ATTACAGACTTGGGGCTGGCTCGGCTGCTGGACATTTGACGAGACAGAGTACCATGCAGAT 2814
Qy 653 ----- 653
Db 2815 GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCGCGGTTCACC 2874
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Db 2875 CACCAGAGTATGTGTGGAGTTATGGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCC 2934
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Qy 653 ----- 653
Db 2995 CTGCCCCAGCCCCCATCTGCACCATGATGTCTACATGATCATGTGTCAAATGTTGGATG 3054
Qy 653 ----- 653
Db 3055 ATTGACTCTGAATGTCCGCCAAGATTCGGGAGTTGGTGTCTGAATTTCTCCGCATGGCC 3114
Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3115 AGGGACCCCGAGCGCTTTGTGGTCAATCCAGAACTGAGGACTTGGGCCCGCAGTCCCTTG 3174
Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAsAla 684
Db 3175 GACAGCACCTTCTACCCCTCACTGCTGAGAGCATGACATGGGGGACCTGTGTGATGCT 3234
Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyValaGly 704
Db 3235 GAGGAGTATCTGGTACCCAGAGGGCTTCTTCTGTCCAGACCTTGCCCGCGGCGCTGGG 3294
Qy 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyAspLeuThr 724
Db 3295 GGCATGGTCCACACAGGCACCGCAGCTCATCTACAGGAGTGGCGGTGGGACCTGCACA 3354
Qy 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3355 CTAGGGCTGAGAGCCCTCTGAAGAGAGAGGCCCCCAAGGCTTCCATGGCACCTCCGAAAGG 3414
Qy 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
Db 3415 GCTGGCTCCGATATTTGATGTGTACCTGGGAATGGGGAGCCCAAGGGGCTGCANAGC 3474
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Qy 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
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Qy 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3535 CCTCTGAGACTGATGGCTAGCTTGCCTCCCTTGCAGCTGAGAGGAGGAGGCTGATG 3594
Qy 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3595 AACCCAGCCAGATGTTGGGCCCGAGCCCTTGCCTCCCGAGAGGGCCCTCTGCTGCTGCC 3654
Qy 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3655 CGACCTGTGTGCCACTCTGGAAAGGCCCAAGACTCTCTCCCCAGGGAGAAATGGGGTC 3714
Qy 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3715 GTCAAGACGTTTTTTCCTTTGGGGGTGCGTGGAGAACCCCGAGTACTTGACACCCAG 3774
Qy 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3775 GGAGAGCTGCCCTCTCAGCCCGCCCTCTCTCTGCTTTCAGCCCGAGCCTTCGACACCTC 3834
Qy 885 TyrTyrTrpAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3835 TATTACTGGACACAGGACCCACAGCGGGGGCTCCACCCAGCACCTTCAAGAGGACA 3894
Qy 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3895 CCTACGGCAGAGAACCCAGAGTACTTGGGTCTGGACGTGCCAGTG 3939
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RESULT 7

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US-10-207-655-44
; Sequence 44: Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069, 401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 44
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-207-655-44
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Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 15 Gaps: 1
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US-09-493-480-6 (1-919) x US-10-207-655-44 (1-4473)

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Qy 1 MetGluLeuAlaAlaLeuCysArgTyrGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
Db 175 ATGGAGCTGGCGGCTTGTGCGCTGGGGGTCTCTCTCGCCCTCTTGGCCCCCGGAGCC 234
Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 235 GCGAGACCCCAAGTGTGACCGCACAGACATGAAGCTGCGGCTCCCTTGCCTAGTCCCAG 294
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 295 ACCCACCTGGACATGCTCCGCCACTCTTACACAGGGCTGCCAGTGGTGTGAGGAAACCTG 354
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Qy	61	GlulLeuThrTyrValLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal	80
Db	355	GAACCTACCTACCTGCCACCAATGCCAGGCTGTCTTCTCGCAGATATCCAGGAGTGTG	414
Qy	81	GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100
Db	415	CAGGGCTACGTGTCTATCGCTCAACCAAGTCAGGCAGGTCCCACTGCAGAGGCTGCCG	474
Qy	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspGlnGly	120
Db	475	ATTGTGCGAGGCACCCAGCTCTTTGAGGACAACTATGCGCTGGCCGTGTGTAGCAATGGA	534
Qy	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGlnLeu	140
Db	535	GACCCGCTGAACAAATACACCCCTGTCAAGGGGCTCCCCAGAGAGGCTTGGGGAGCTGTG	594
Qy	141	GlnLeuArgSerLeuThrGluIleLeuLeuGlyGlyValLeuIleGlnArgAsnProGln	160
Db	595	CAGCTTCGAAGCCTCACAGAGATCTTGAAAGGAGGGGTCTTGATCCAGGGAAACCCCCAG	654
Qy	161	LeuCysTyrGlnAspThrIleLeuTrpIlyAspIlePheHisIlyAsnAsnGlnLeuAla	180
Db	655	CTCTGCTACCAAGACACGATTTTGTGCAAGACATCTTCCACAAGAACCAACCAAGCTGGCT	714
Qy	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
Db	715	CTCACCTGATAGACACAAACCGCTCTCGGGCCCTGCCACCCCTGTCTCCGATGTGTAAAG	774
Qy	201	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220
Db	775	GGCTCCCGCTGCTGGGAGAGAGATTCTGAGGATGTTCAGAGCCTGACGGGCACGTGCTGT	834
Qy	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys	240
Db	835	GCCGGTGGCTGTGCTGCCCTGCAAGGGGCCACTGCCCCACTGACTGCTGCCATGAGCAGTGT	894
Qy	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
Db	895	GCTGCCGGCTGCAACGGGCCCCAAGCATCTGTGACTGCTGGCTGCCCTCCACTTCACACCAC	954
Qy	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280
Db	955	AGTGGCATCTGTGAGCTGCATGCTGCCAGCCCTGTGTCACTACACACAGACACGTTTGAG	1014
Qy	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300
Db	1015	TCCATGCCCAATCCGAGGGCGGTATACATTCGGGGCCAGCTGTGTGACTGCTGTGCC	1074
Qy	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
Db	1075	TACAACTACCTTTCTAOCGAAGTGGGATCTCTGCACCTCTGTCTGCCCTTGCACACACAA	1134
Qy	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340
Db	1135	CAGGTACAGCAGCAGGATGGAACACAGCGGTGTGAGAAGTGCACCAAGCCCTGTGCCCGA	1194
Qy	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
Db	1195	GTGTGCTATGTCTGGGCATGGAGCCTTGCAGAGGTGAGGGCAGTTTACCAAGTGCACAT	1254
Qy	361	IleGlnGluPheAlaGlyCysIlyValIlePheGlySerLeuAlaPheLeuProGluSer	380
Db	1255	ATCCAGAGATTTGTCTGGCTGCAAGAAGATCTTTGGAGCCCTGGCATTTCTGCGGAGAGC	1314
Qy	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400
Db	1315	TTTGATGGGGACCCAGCTTCCAACTGCCCGCTTCCAGCCAGCAGCAGCTTCCAAGTGT	1374
Qy	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	420
Db	1375	GAGACTCTGGAAGAGATCACAGTTTACCTATACATCTCAGCATGGCCGAGCAGCTGCTCT	1434

Qy	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyValAla	440
Db	1435	GACCTCAGCGTCTTCAGAACTGCAAGTAATCCGGGGACGAATTCCTGCACAATGGCGCC	1494
Qy	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
Db	1495	TACTCGGTGACCTTCGAAGGGCTGGGGCATCAGCTGGCTGGGGCTGGCGCTCACTGAGGGAA	1554
Qy	461	LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal	480
Db	1555	CTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCACCTCTGCTTGTGTGCACACGGTG	1614
Qy	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
Db	1615	CCCTGGACACAGCTCTTTCGGAACCCCGACCAAGCTCTGCTCCACACTGTCACCAACCGGCCA	1674
Qy	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
Db	1675	GAGACCAAGTGTGTGGCGGAGGGCTGGCTGCCACCACTGTGGCCCCGAGGGCACTGC	1734
Qy	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
Db	1735	TGGGGTCCAGGGCCACCAGTGTGTCACTCAGCCAGTTCCTTCGGGGCCAGGAGTGC	1794
Qy	541	ValGluGluCysArgValLeuGlnGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560
Db	1795	GTGGAGGAATGCCGAGTACTGCAGGGGCTCCCGAGGAGTATGTGAATGTCAGGCACTGT	1854
Qy	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
Db	1855	TTGCCGTGCCACCTGTAGTGTCAAGCCCGACGAATGGCTCAGTGACCTCTTTTGGACCCGGAG	1914
Qy	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys	600
Db	1915	GCTGACCAAGTGTGGCTGTGGCCACTATAAGGACCCTCCCTCTCGTGGCCCGCTGC	1974
Qy	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu	620
Db	1975	CCCAGCGTGTGAACCTGACCTCTCTCTACATGCCACTCTGGAAGTTTCAGATGAGGAG	2034
Qy	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640
Db	2035	GGCGCATGCCACCTTGGCCCATCACTGCACCCACTCTCTGTGTGGACCTGGATGACAG	2094
Qy	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
Db	2095	GGCTCCCCCGGAGCAGAGACGACGCCCTCTGAGTCCATCATCTCTCGGGTGGTTGGC	2154
Qy	653	-----	653
Db	2155	ATTCTGCTGGTGGTCTTGGGGTGGTCTTGGGATCTCTCATCAGCCACGCCAGCAG	2214
Qy	653	-----	653
Db	2215	AAGATCCGGAAGTACAGATCGGAGACTGCTGCAGGAAACGGAGCTGTGTGGACCGCGTG	2274
Qy	653	-----	653
Db	2275	ACACTAGCGGAGCGATGCCCAACAGCGCGCAGATGGCGATCTCTGAAGAGACGGAGCTG	2334
Qy	653	-----	653
Db	2335	AGGAAGTGAAGTGTCTTGGATCTGGCGCTTTTGGCACAGTCTACAGGGCATCTGGATC	2394
Qy	653	-----	653
Db	2395	CCTGTATGGGGAATGTGAAAAATTCAGTGGCCATCAAGAGTGTGTGAGGGAAACACATCC	2454
Qy	653	-----	653
Db	2455	CCCAAGCCAAAGAAAAATTTAGACGACGACATACGTGATGGCTGTGTGGCTCCCCA	2514
Qy	653	-----	653

Qy	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120
Db	475	ATTGTGCGAGGCACCCAGCTCTTTGAGGACAACACTATGCCCCCTGGCCGTGTAGACAATGGA	534
Qy	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140
Db	535	GACCCGCTGAACAATAACACCCCTGTCCACAGGGGCGCTCCCCAGAGGCGCTGCGGGAGCTG	594
Qy	141	GlnLeuArgSerLeuThrGluLeuLeuLysGlyValLeuIleGlnArgAsnProGln	160
Db	595	CAGCTTCGAGGCTCACAGAGATCTTGAAAGAGGGGTCTTGATCCAGCGGACACCCCCAG	654
Qy	161	LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnGlnLeuAla	180
Db	655	CTCTGCTACCAGGACACGATTTTGTGAAGGACATCTTCCACAAGAACACACAGCTGGCT	714
Qy	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
Db	715	CTCACACTGATAGACACCAACCGCTCTCGGGGCTGCCACCCCTGTTCCTCGATGTGTAA	774
Qy	201	GlySerArgCysTyrGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220
Db	775	GGCTCCCGCTGCTGGGAGAGAGATTCTGAGGATGTTCAGAGCTTCAGCGGCATCTCTGT	834
Qy	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	240
Db	835	GCCGTTGGCTGTGCCCCGTGCAAGGGGCCACTGCCCACTGACTGCTGCCATGAGCAGTGT	894
Qy	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
Db	895	GCTCCCGGCTGCACGGGCCCCAAGCACTCTGACTGCCCTGGCTGCCCTTCACATTCACACC	954
Qy	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280
Db	955	AGTGGCATCTGTGAGCTGCACCTGCCAGCCCTGTGTCACTACACACACGACACGTTTGAG	1014
Qy	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300
Db	1015	TCCATGCCCAATCCCGAGGGCCGATATACATTGGCGGCCAGCTGTGTGACTGTGCTGCC	1074
Qy	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
Db	1075	TACAACTACCTTTCTAGCGAGCTGGGATCTCTGCACCTCTGTCTGCCCTTCGCACACCAA	1134
Qy	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340
Db	1135	GAGGTGACGACAGAGATGGAAACACAGCGGTGTGGAAGTGCACAGAGCCCTGTGCCCGA	1194
Qy	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
Db	1195	GTGTGCTATGCTCTGGGCATGGAGCCTTGCAGAGGTGAGGGCAGTTACAGTGCCCAAT	1254
Qy	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380
Db	1255	ATCCAGGAGTGTGTGCTGCGAAGAAGATCTTTGGGAGCCTGGCGATTTCTGCCGGAGAGC	1314
Qy	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400
Db	1315	TTTGATGGGGACCCAGCCCTCCACACTGCCCCCGCTCCAGCCAGAGAGAGCTCCAAAGTGT	1374
Qy	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro	420
Db	1375	GAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGGACAGCTCGCT	1434
Qy	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440
Db	1435	GACCTCAGCGTCTTCCAGAACCTCGCAAGTAAATCCGGGGAGCGAATTTCTGCACAAATGG	1494
Qy	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuGlyLeuArgSerLeuArgGlu	460
Db	1495	TACTCGCTGACCTGCACAGGCGCTGGGCATCAGCTGGCTGGGGCTGGCTCACTGAGGGAA	1554
Qy	461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480

Qy	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120
Db	475	ATTGTGCGAGGCAACCAGCTCTTTGAGGACAACACTATGTCCCTGCGCGTGTAGACAATGGA	534
Qy	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140
Db	535	GACCCGCTGAACAATAACACCCCTGTCCACAGGGGCGCTCCCCAGAGGCGCTGCGGGAGCTG	594
Qy	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln	160
Db	595	CAGCTTCGAGGCTCACAGAGATCTTGAAAGAGGGGTCTTGATCCAGCGGACACCCCCAG	654
Qy	161	LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnGlnLeuAla	180
Db	655	CTCTGCTACCAGGACACGATTTTGTGAAGGACATCTTCCACAAGAACACACAGCTGGCT	714
Qy	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
Db	715	CTCACACTGATAGACACCAACCGCTCTCGGGGCTGCCACCCCTGTTCCTCGATGTGTAA	774
Qy	201	GlySerArgCysTyrGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220
Db	775	GGCTCCCGCTGCTGGGAGAGAGATTCTGAGGATGTTCAGAGCCTGACGCGCATCTCTGT	834
Qy	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	240
Db	835	GCCGTTGGCTGTGCGCGCTGCAAGGGGCCACTGCCCACTGACTGCTGCCATGAGCAGTGT	894
Qy	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
Db	895	GCTCGCGGCTGCACGCGGCCCAAGCATCTTGACTGCGCTGGCTGCCCTTCCACTTCAACCC	954
Qy	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280
Db	955	AGTGGCATCTGTGAGCTGCACCTGCCAGCCCTGTGTCACTCACACACGACACAGTTTGAG	1014
Qy	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300
Db	1015	TCCATGCCCAATCCCGAGGGCGGTATACATTGGCGGCCAGCTGTGTGACTGTCTGTCCC	1074
Qy	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
Db	1075	TACAACCTACCTTCTACGAGCTGGGATCTCTGCACCTCTGTCTGCCCTTGCACACACAA	1134
Qy	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340
Db	1135	GAGGTGACGACAGAGATGGAACACAGCGGTGTGGAAGTGCACAGAGCCCTGTGCCCGA	1194
Qy	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
Db	1195	GTGTCTATGTCTGGGCATGGAGCCTTGCAGAGGTGAGGGCAGTTACAGTGCCCAAT	1254
Qy	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380
Db	1255	ATCCAGGAGTGTGTGGCTGCAAGAAGATCTTTGGGAGCCTGGGCAATTTCTGCCGAGAGC	1314
Qy	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400
Db	1315	TTTGATGGGGACCCAGCCCTCCACACTGCCCCCGCTCCAGCCAGAGAGCTCCCAAGTGT	1374
Qy	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro	420
Db	1375	GAGACTCTGGAAGAGATCACAGGTATACCTATACATCTCAGCATGGCCGGAAGCTCGCT	1434
Qy	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440
Db	1435	GACCTCAGCGTCTTCCAGAACCTTCGAGTAAATCCGGGGAGCAATTTCTGCACAATGGCGCC	1494
Qy	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuGlyLeuArgSerLeuArgGlu	460
Db	1495	TACTCGCTGACCTGCACAGGCGTGGGCATCAGCTGGCTGGGGCTGGCTCACTGAGGGAA	1554
Qy	461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480

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Qy	665	ASP	SerThr	Phe	Thr	Arg	Ser	Leu	Leu	Ala	Asp	Met	Gly	Asp	Leu	Val	Asp	Ala	684			
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Qy	685	GLU	Glu	Thr	Leu	Val	Pro	Gln	Gln	Gly	Phe	Phe	Cys	Pro	Asp	Pro	Ala	Pro	Gly	Ala	Gly	704
Db	3235	GAG	AGATAT	CTG	GTAC	CCG	ACG	AGG	CTTCT	TGTCA	GAC	CCCTG	CCCGGG	CGCTGGG	3294							
Qy	705	GLY	Met	Val	His	Arg	His	Arg	Ser	Ser	Ser	Thr	Arg	Ser	Gly	Gly	Gly	Asp	Leu	Thr	724	
Db	3295	GGC	ATG	TCC	ACCA	CAG	CA	CCG	CAG	CTCAT	TAC	CA	GAG	GTGG	CGTGG	GGAC	CTG	CA	3354			
Qy	725	LEU	Gly	Leu	Glu	Pro	Ser	Glu	Glu	Glu	Ala	Pro	Arg	Ser	Pro	Leu	Ala	Pro	Ser	Glu	Gly	744
Db	3355	CTA	GGCTGG	AGCCCT	CTG	AAG	AGG	AGG	CCGCC	CAG	GTCTC	CA	CTG	GG	CA	CCCTCCG	AA	GGG	3414			
Qy	745	ALA	Gly	Ser	Asp	Val	Phe	Asp	Gly	Asp	Leu	Met	Gly	Ala	Ala	Val	Ser	Gly	Leu	Gln	Ser	764
Db	3415	GCT	GGCTCC	CGATG	TATTT	GA	TGTG	TG	TGAC	CTG	GGAA	TGG	GGG	CAG	CCA	AGG	GGCTG	CA	AA	AGC	3474	
Qy	765	LEU	Pro	Thr	His	Asp	Pro	Ser	Pro	Leu	Gln	Arg	Tyr	Ser	Glu	Asp	Pro	Thr	Val	Pro	Leu	784
Db	3475	CTC	CCC	CA	CAT	GA	CCCC	CAG	CCCTCT	AC	AG	GGGTAC	AGT	GAG	GA	CCCC	CA	GAT	AC	CCCTG	3534	
Qy	785	PRO	Ser	Glu	Thr	Asp	Gly	Tyr	Val	Ala	Pro	Leu	Thr	Cys	Ser	Pro	Gln	Pro	Glu	Tyr	Val	804
Db	3535	CC	CTCTG	AGACT	GTATG	GTAC	TTG	TG	CCCC	CTG	ACCTG	CA	GG	CCCC	CA	GG	CCCTG	GA	TAT	GTG	3594	
Qy	805	ASN	Gln	Pro	Asp	Val	Arg	Pro	Gln	Pro	Pro	Ser	Pro	Arg	Glu	Gly	Pro	Leu	Pro	Ala	Ala	824
Db	3595	AAC	CAG	CCAG	ATG	TGTGG	CC	CC	CA	CCCTT	CG	CC	CCG	AG	AGG	GG	CCCTCT	CT	CG	CTG	CTG	3654

Qy	865	GlyGlyAlaalaProGlnProHisProProProAlaPheSerProAlaPheAspAsnLeu	884
Db	3775	GGAGGAGCTCCCTTCAGCCCCACCTCTCTCCTTTCAGCCAGCTTCGACAACCTC	3834
Qy	885	TyrTyrtiraspGlnaspProProGluArgGlyAlaProProSerThrPheLysGlyThr	904
Db	3835	TATTACTGGAGCACGAGACCACCAGAGCGGGGGCTCCACCCAGACCTTCMAAGGACA	3894
Qy	905	ProThralaGluasnProGluTyrltyrLeuGlyLeuasppalProVal	919
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RESULT 9

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US-10-207-498-5
; Sequence 5, Application US/10207498
; Publication No. US20030143568A1
; GENERAL INFORMATION:
; APPLICANT: Elizabeth Singer
; APPLICANT: Ralf Landgraf
; APPLICANT: Dennis J. Slamon
; APPLICANT: David Eisenberg
; TITLE OF INVENTION: METHODS AND MATERIALS FOR CHARACTERIZING
; TITLE OF INVENTION: AND MODULATING INTERACTIONS BETWEEN HEREGULIN AND HER3
; FILE REFERENCE: 30448.103-US-01
; CURRENT APPLICATION NUMBER: US/10/207,498
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/308,431
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3765
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-10-207-498-5

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Db 2941 AGGGACCCCGCGCTTTGTGTGTCATCCAGATGAGGACTTGGSCCCAGCCAGTCCCTTG 3000
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Qy 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
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RESULT 10
US-09-811-123-8
; Sequence 8, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
; APPLICANT: Ralph Schwall
; APPLICANT: Mark Sliwowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ERBB
; TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
; FILE REFERENCE: GENENT.073A2
; CURRENT APPLICATION NUMBER: US/09/811.123
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-123-8

Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 9 Gaps: 1

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Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
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Db 181 GNACTCACTTACCTGCCCCCAATGCCAGCGCTGCTCTCTCTGAGGATATCCAGGAGGTG 240
Qy 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
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Qy 865 GlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAspAsnLeu 884
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Qy 885 TyrTyrTyrAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3661 TATTACTGGGACCGAGGACCCACGAGCGGGGCTCCACCCAGCACCTTCAAGGGGACA 3720
Qy 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3721 CCTACGCGCAGAGAACCCAGTACTTGGGTCTGGAGCTGGCCAGTG 3765

RESULT 12

US-09-984-092-3

; Sequence 3, Application US/09984092

; Publication No. US20040037840A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL THERAPEUTIC VACCINE FORMULATIONS
; FILE REFERENCE: P101PC00
; CURRENT APPLICATION NUMBER: US/09/984,092
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3768)
US-09-984-092-3

Alignment Scores:

Pred. No.:	0	Length:	3768
Score:	4892.00	Matches:	918
Percent Similarity:	73.15%	Conservative:	0
Best Local Similarity:	73.15%	Mismatches:	1
Query Match:	96.34%	Indels:	336
DB:	13	Gaps:	1

US-09-493-480-6 (1-919) x US-09-984-092-3 (1-3768)

Qy	1	MetGluLeuAlaAlaLeuCysArgTTPGlyLeuLeuLeuAlaLeuLeuProGlyAla	20
Db	1	ATGAGCTGGGGCTTTGTGCCCTGGGGCTCTCTCTCGCCCTTTCCTCCCGGAGCC	60
Qy	21	AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu	40
Db	61	GGAGACCCAGTGTGACCGGACAGACATGAGCTCGGCTCCCTGCCAGTCCCGAG	120
Qy	41	ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu	60
Db	121	ACCACCTGGACATGCTCGGCACCTCTTACCAGGGCTGCCAGGTGGTGAGGAAACCTG	180
Qy	61	GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal	80
Db	181	GAACTCACTACCTGGCCCAATGCCAGCGCTGCTCTTCTGACAGATATCCAGGAGTG	240
Qy	81	GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100
Db	241	CAGGGCTAGTGTCTATCGCTCACACCAAGTAGGAGGAGTCCCACTGCAGAGGCTGGCG	300
Qy	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120
Db	301	ATTGTGGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGGCGCTGTAGACAAATGGA	360
Qy	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140
Db	361	GACCCGCTGAACAATATACCCCTGTCAAGGGGCTTCCCGAGAGGCTTCGGGAGCTG	420
Qy	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln	160
Db	421	CAGCTTCAGAGCTCACAGAGATCTTGAAGAGGGGTCTTGATCCAGCGAAGCCCGAG	480
Qy	161	LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnAsnGlnLeuAla	180
Db	481	CTCTGTACCCAGGACACGATTTTGTGGAAGGACATCTTCCACAAGAACCAACAGCTGGCT	540
Qy	181	LeuThrIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
Db	541	CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTTCCCATGTGTAAAG	600
Qy	201	GlySerArgCysTyrGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220
Db	601	GGCTCCCGCTGCTGGGGAGAGAGTTCTGAGGATTTCTAGAGCTTGTACAGCCTGACCGCATCTCTGT	660
Qy	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys	240


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Db 2881 ATTGACTCTGAATGTCGGCAAGATTCCCGGAGTGGTGTCTGAATTTCTCCCGCATGGCC 2940
QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGGACCCCGCGCTTTGGTTCATCCAGANTGAGGACTTGGCCCGCAGTCCTCTTG 3000
QY 665 AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGACCTGTGGTGTCT 3060
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGTGTACCCAGCGAGGGCTTCTGTCTCAGACCTTGCCTCCCGCGCTGGG 3120
QY 705 GlyMetValHisHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
Db 3121 GGATGTGTCACACACAGGACCCGAGCTCATCTACACAGGAGTGGCGTGGGGACCTGACA 3180
QY 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3181 CTAGGCTGGAGCCCTCTGAAGAGGAGGCCCCCGAGTCTCCACTGGCACCTTCGAGGG 3240
QY 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaGlyGlyLeuGlnSer 764
Db 3241 GCTGGCTCCGATGATTTGATGTGACCTGGGAATGGGGCAGCCCAAGGGCTGCCAAGC 3300
QY 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 3301 CTTCCACACATGACCCCGCCCTCTACACGGGTACAGTGAGGACCCCAACAGTACCCCTG 3360
QY 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3361 CCCTCTGAGACTGATGCTAGTGTGCTCCCGCCCTGACCTGCAGCCCCCAGCCCTGAATGTG 3420
QY 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3421 AACACGCCAGATGTTGGGCCCGCCAGCCCTTCCGCCCGAGAGGGCCCTCTGCTGTGCTG 3480
QY 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3481 CGACCTGCTGTGCTGCTCTGGAAGGGCCAGACTCTCTCCCGAGGAGAGATGGGTC 3540
QY 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3541 GTCAAGACGTTTTTGCCTTTGGGGGTGCGGTGAGAACCCCGAGTACTTGACACCCCGAG 3600
QY 865 GlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3601 GGAGGAGCTGCCCTCAGCCCGCCACCTCTCTCTGCTTCCGCTTCCAGCCAGCTTCGACACCTC 3660
QY 885 TyrTyrTyrAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3661 TATTACTGGACACGAGGACCCACGAGCGGGGCTCCACCCAGACCTTTCAGAGGACA 3720
QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3721 CCTACGGCAGAGAACCCAGAGTACCTGGGTCTGGAGTGGCCAGTG 3765
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RESULT 13

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US-10-280-576-3
; Sequence 3, Application US/10280576
; Publication No. US2004004405A1
; GENERAL INFORMATION:
; APPLICANT: Wolff, Matthew R.
; TITLE OF INVENTION: VASCULAR STENT OR GRAFT COATED OR IMPREGNATED WITH PROTEIN
; FILE REFERENCE: 09820.189
; CURRENT APPLICATION NUMBER: US/10/280,576
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 60/343,732
; PRIOR FILING DATE: 2001-10-25
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; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 3
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; LENGTH: 3768
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; TYPE: DNA
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; ORGANISM: Homo sapiens
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US-10-280-576-3
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Alignment Scores:

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Pred. No.: 0 Length: 3768
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 13 Gaps: 1
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US-09-493-480-6 (1-919) x US-10-280-576-3 (1-3768)
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QY 1 MetGluLeuAlaLeuCysArgTTPGlyLeuLeuAlaLeuLeuProGlyAla 20
Db 1 ATGGAGCTGGCGGCTTTGTGCGCTGGGGGCTCTCTCGCCCTTTGCCCGGAGGCC 60
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 61 GCAGACACCCAGTGTGCACCGGCACAGACATGAGGTGGGCTCTCTGCCAGTCCCAG 120
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 121 ACCACCTGACATGCTCCGCCACCTCTACCCAGGGCTGCCAGGTGGTGACGGAAACCTG 180
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnIleVal 80
Db 181 GAATCTACCTTACCTGCGCCACCAATGCCAGCTGTCTCTCTGCCAGGATATCCAGGAGTG 240
QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 CAGGGCTACGTGCTCATCGCTCACACCAAGTAGGAGGAGGTCCCACTGCAGAGGCTGG 300
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 301 ATTGTGCGAGGCCACCCAGCTCTTTGAGGACAACTATATGCCCTGGCGCTCTAGACAAATG 360
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 361 GACCCCTGAAACAATAATACCACTGTCACAGGGGCTCTCCCGAGGAGGCTCTGGGAGCTG 420
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 421 CAGCTTCGAGCCTTCACAGAGATCTTGAAGAGGAGGGGTCTTGATCCAGCGGAAACCCCG 480
QY 161 LeuCysTyrGlnAspThrIleLeuThrLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 481 CTCTGCTCACCGACACGATTTTGTGAGAGGACATCTTCCACAGAACCAACAGCTGGCT 540
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisAspCysSerProMetCysLys 200
Db 541 CTCACTGATAGACACCAACCCCTCTCGGGGCTTGCACCCCTGTCTTCCGANTGTGTAG 600
QY 201 GlySerArgCysTyrGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 601 GGCTCCCGCTGCTGGGGAGAGAGTCTGTAGGATTTGTAGAGCTGTGACAGGCTTGACGGCTGT 660
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
Db 661 GCGGTGGCTGTGCTCCGCTGCAGAGGGGCCACTGCCCACTGACTGCTGCCATGAGCAGTGT 720
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 721 GCTGCCGGCTGCACGGGGCCCCAAGCACTCTGACTGCTGGCTGCCCTCCACTTCCACAC 780
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 781 AGTGGCATCTGTGAGCTGGCACTGCCCGCCCTGTGTCACTACACACACAGACAGCTTTGAG 840
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281 SerMetProAnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
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841 TCCATGCCCATCCGAGGCGGTATACATTTGGCGCCAGCTGTGTGACTGCTGTCCC 900
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301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
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901 TACAACACTACCTTTCTACCGAGCTGGATCCCTGCAACCTCTGCTGCCCTGCAACACAA 960
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321 GlnValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
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341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
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1201 GAGACTCTGGAGAGATCACAGTTTACCTATACATCTCAGCATGGCCGAGCAGCTGCGCT 1260
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421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
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1261 GACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGAGCAGAAATCTGCACAAATGGCGCC 1320
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1321 TACTCGCTGACCTCTGCAAGGGCTGGGCATCAGCTGGCTGGGCTGCGCTCACTAGAGGAA 1380
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|
461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
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1441 CCTTGGGACCAAGCTCTTTGGGAACCGCACCAAGCTCTGCTCCACACTGCCAACCGGCCA 1500
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501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
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1501 GAGGACGAGTGTGTGGGCGAGGECCTGGCTTCCACCAAGCTGTGCCCGAGGGCACTGC 1560
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541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
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1621 GTGGAGGAATGCCGAGTCTGACGAGGGCTCCCGAGGGAGTATGTGAATGCCAGGCACTGT 1680
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561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
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1681 TTGCGGTGCACCTCTGAGTGTGAGGCCAGAGATGGCTCAGTGACCTGTGTGAGCGGAG 1740
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581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
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1741 GCTGACCAAGTGTGGCTGTGCCACATATAGGACCTCTCTTCTGGGTGGCCCGCTGC 1800
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601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
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1801 CCCAGCGGTGAAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG 1860
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621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
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1861 GCGCATGTCAGCCTTGGCCCATCAACTGACCCACTCTCTGTGTGGACCTGTGATGCAAG 1920

641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
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1921 GGTCGCCCGCCGAGCAGAGAGCCAGCCCTCTGAGCTCCATGCTCTCTCGCGTGTGGC 1980
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653 ----- 653
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1981 ATTCTGTGTGTCGTGGTCTTGGGGGTGTCTTTTGGGATCCTCATCAAGCGACGGCAGCAG 2040
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653 ----- 653
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2041 AAGATCCGGAAGTACACGATCGGAGACTGCTGCAGGAAACGGAGCTGTGTGAGCGCTG 2100
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2101 ACACCTAGCGAGCGATGCCCAACGAGCGCAGATGGGATCTCTGAAAGAGAGCGAGCTG 2160
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2161 AGGAAGGTGAAGGTGCTTGGATCTGGCCCTTTTGGCACAGTCTACAGGGCATCTGGATC 2220
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653 ----- 653
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654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
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2941 AGGGAACCCAGCGCTTTGTGTGTCTATCCAGAAATGAGGACTTGGGCCCGAGCCAGTCCCTTG 3000
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665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684

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QY 725 LeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGluGly 744
DB 3181 CTAGGGCTGGAGCCCTCTGAAGAGGAGGCCGCCAGGTCTCCATCTGCGACCTCCGAAGG 3240
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DB 3721 CCTACGGCAGAGAACCACAGAGTACTTGGGGTCTGGACGTGCCAGTG 3765
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RESULT 14

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US-09-877-177-11
; Sequence 11, Application US/09877177
; Publication No. US20020192652A1
; GENERAL INFORMATION:
; APPLICANT: Peter V. Danenberg et al.
; TITLE OF INVENTION: Method of determining Epidermal Growth
; TITLE OF INVENTION: Factor Receptor and HER2-New Gene Expression
; FILE REFERENCE: 11220/120
; CURRENT APPLICATION NUMBER: US/09/877,177
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-877-177-11
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Alignment Scores: 0 Length: 4530
Pred. No.: 4892.00 Matches: 918
Score:
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Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 93.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 9 Gaps: 1
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US-09-493-480-6 (1-919) x US-09-877-177-11 (1-4530)

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QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
DB 211 GCAGACACCCAGGTGTGACCGGCACAGACATGAAGCTGGGCTCCCTTGCAGTCCCGAG 270
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlnAsnLeu 60
DB 271 ACCACCTGGACATGCTCCCGCACCTCTACAGGGCTGCCAGGTGGTGAGGGAACCTG 330
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspPheGlnGluVal 80
DB 331 GAATCTCACCTTACCTGCGCCACCAATGCCAGCTGTCTCTTCTGCAAGGATATCCAGAGGTG 390
QY 81 GlnGlyTyrValLeuLeuAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
DB 391 CAGGGCTACGTGTCTATCGCTCAACCAAGTGAAGGAGGTCCCTCTGCGAGGGCTGGCG 450
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
DB 451 ATTGTGCGAGGACCCAGCTCTTTGAGACAACTATGCTCCCTGGCGGTGTAGACAATGGA 510
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
DB 511 GACCCGCTGAACAAATACACCCCTGTCAAGGGGCTCCCGAGAGGCTCCGCGAGGTG 570
QY 141 GlnLeuArgSerLeuThrGluLeuLysGlyValLeuLeuGlnArgAsnProGln 160
DB 571 CAGCTCGAAGCCCTCAGAGATCTTGAAGAGGGGTCTTGATCCAGCGGAGACCCCGAG 630
QY 161 LeuCystyrGlnAspThrIleLeuTyrLysAspPhePheHisLysAsnAsnGlnLeuAla 180
DB 631 CTCTGTCTACCGAGCAGCATTTTGTGAAGGACATCTTCCACAAGAACCAACAGCTGGCT 690
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
DB 691 CTCACATGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTCCGATGTGTAAAG 750
QY 201 GlySerArgCysTyrGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
DB 751 GGTCTCCGCTGTCTGGGAGAGAGTTCAGAGATTGTTCAGAGCCTGACGGCACTGTCTGT 810
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
DB 811 GCCGTGGCTGTGCCGCTGCAAGGGGCCACTGCGCCACTGACTGCTGCATGAGCAGTGT 870
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
DB 871 GCTGCGGGCTGCAGCGGCCCAAGACTCTGAGCTGCTGGCTGCGCTGCCCTTCAACCCAC 930
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
DB 931 AGTGGCATCTGTGAGCTGCACTGCCAGCCCTGGTCACTTACACACACAGACACCGTTTGA 990
QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
DB 991 TCCATGCCCAATCCGAGGGCCGATATACATTCGGCGCCAGCTGTGTGACTGCTGTCTCC 1050
QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
DB 1051 TACAACCTACCTTTCTAGCGGACGTGGGATCTCGCACCTCTGCTGCCCCCTGCACACAC 1110
QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
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Db 1111 GAGGTGACAGCAGGATGGAACACAGCGGTGTGAGAGTGCAGCAAGCCCTGTGCCGA 1170
Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
Db 1171 GTGCTATGCTCTGGGCAATGAGCACTTGGCAGAGGTGAGCGCAGTTTACCAAGTCCCAAT 1230
Qy 361 IleGlnGluPheAlaGlyCysIleValPheGlySerLeuAlaPheLeuProGluSer 380
Db 1231 ATCCAGGAGTTTGGCTGCAAGAGATCTTTGGGAGCCTGGCAATTTCTGCCGAGAGC 1290
Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe 400
Db 1291 TTTGATGGGACCCAGCCTCCACACTGCCCGCTCCAGCCAGAGCAGCTCCCAAGTGT 1350
Qy 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420
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Qy 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
Db 1411 GACCTCAGCGTCTTCAGAACCTGCAGTAATCCGGGAGCAATTTCTGCACANTGGCGC 1470
Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
Db 1471 TACTCGCTGACCTGCAGAGGCTGGGCATCAGCTGGCTGGGCTGGCTCACTGAGGGA 1530
Qy 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
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Qy 501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
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Qy 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
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Qy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
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Qy 601 ProSerGlyValLysProPheLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
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Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
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Qy 653 ----- 653
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Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3091 AGGGAACCCCGAGCGCTTTGTGTGTCATCCAGAAATGAGGACTTGGGCGCCAGCAGTCCCTTG 3150
Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
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Qy 685 GluGluTyrLeuValProGlnGlnPheCysProAspProAlaProGlyAlaGly 704
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Qy 705 GlyMetValHisHisArgHisArgSerSerSerThrArgSerGlyGlyGlyAspLeuThr 724
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RESULT 15

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; Publication No. US20030224993A1
; GENERAL INFORMATION:
; APPLICANT: Land, Hartmut
; APPLICANT: Deleu, Laurent
; TITLE OF INVENTION: COMPOSITIONS THAT INHIBIT PROLIFERATION
; TITLE OF INVENTION: OF CANCER CELLS
; FILE REFERENCE: 21108.000503
; CURRENT APPLICATION NUMBER: US/10/392.113
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: 60/365,078
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: PCT/US01/32127
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/239,705
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
US-10-392-113-45
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Alignment Scores:

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Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
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Query Match: 96.34% Indels: 336
DB: 13 Gaps: 1
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QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 211 GCAGACACCCAGTGTGCACCGGCACAGACATGAAGCTGGGCTCCCTTGCAGTCCCGAG 270
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlnAsnLeu 60
Db 271 ACCCACTGGACATGCTCCGCCACTCTACAGGGCTGCCAGGTGGTGGCAGGGAACCTG 330
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 331 GAACCTACCTTACCTGCCACCAATGCCAGCTGTCTCTTCTGTCAGGATATCCAGAGGTG 390
QY 81 GlnGlyTyrValLeuLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
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QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 511 GACCCGTGAACCAATACCACTGTCCAGGGGCTCCCGAGGAGGCTCGGGAGCTG 570
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Db 571 CAGCTTGAAGCTTCACAGAGATCTTGAAGAGGGGTCTTGATCCAGCGGAACCCCCAG 630
QY 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 631 CTCTGTACCCAGCACAGATTTTGTGGAGAGACATCTTCCACAAGAACCAACAGCTGGCT 690
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 691 CTCACATGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTTCCGATGTGAAG 750
QY 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
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QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
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QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
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QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
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QY	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaLeu	360	QY	653	-----	653
DB	1171	GTGCTATGCTGTGGCATGAGCATTGCGAGAGGTGAGGCGCAGTTACCACTGCCAAT	1230	DB	2251	ACACCTAGCGGAGCGATGCCAACCGGCGCAGATCGGGATCTGAAAGAGACGGAGCTG	2310
QY	361	IleGlnGluPheAlaGlyCysIleValPheGlySerLeuAlaPheLeuProGluSer	380	QY	653	-----	653
DB	1231	ATCCAGGAGTTTGTCTGGCTGCAAGAGATCTTTGGGAGCTGGCATTTCTGCCGGAGAGC	1290	DB	2311	AGGAAGTGAAGGTGCTTGGATCTGGGCGCTTTTGGGCACAGTCTCAAGGGCATCTGGATC	2370
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe	400	QY	653	-----	653
DB	1291	TTTGATGGGGACCCAGCTTCCAACTGCTCCCGCTCCAGCCAGAGCAGCTCCAGGTGTTT	1350	DB	2371	CCTGATGGGGAGAAATGTGAAATTTCCAGTGGCCATCAAAAGTGTGTGAGGGAAACACATCC	2430
QY	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro	420	QY	653	-----	653
DB	1351	GAGACTCTGGAAGAGATCACAGTACCTATATACATCTCAGCATGGCCGACAGCCTGCCT	1410	DB	2431	CCCAAAGCCAA CAAGAAATCTTAGAGGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA	2490
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisGlyAla	440	QY	653	-----	653
DB	1411	GACCTCAGCGCTTCCAGAACCTGCAGTAATCCGGGGAGCAATTTCTGCACAATGGCGCC	1470	DB	2491	TATGTCTCCCGCTTCTGGGCATCTGCCTGCATCCACGCTGCAGCTGGTGACACAGCTT	2550
QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuGlyLeuArgSerLeuArgGlu	460	QY	653	-----	653
DB	1471	TACTTGCTGACCTTGCAGGGCTGGGCATCAGCTGGCTGGGGCTGGCTCACTGAGGAA	1530	DB	2551	ATGCCCTATGCTGCTCTTAGACCATGTCCGGGAAACCGCGACGCCCTGGGCTCCAG	2610
QY	461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480	QY	653	-----	653
DB	1531	CTGGGAGTGGAGTGGCTCATCCACCACTAACACCACTCTGCTTCTGTGCACACGGTG	1590	DB	2611	GACCTGCTGAACCTGTGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGGG	2670
QY	481	ProTyrAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500	QY	653	-----	653
DB	1591	CCCTGGGACAGCTCTTTCCGAAACCCGCGACCAAGCTCTGCTCCACAGCTGCCAACCGGCCA	1650	DB	2671	CTCGTACACAGGAGCTTGGCGCTCGGAAAGTGTCTGCTCAAGAGTCCCAACCATGTCAAA	2730
QY	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520	QY	653	-----	653
DB	1651	GAGGACAGTGTGTGGCGAGGGCTGGCTGACCACTGCTGGCGCCGAGGGCACTGC	1710	DB	2731	ATTACAGACTTTCGGGCTGGCTCGGCTCTGGACATTGAACGAGACAGAGTACCATGTCAGAT	2790
QY	521	TyrGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540	QY	653	-----	653
DB	1711	TGGGTCACAGGCCACCCAGTGTGTCACTGAGCGAGTTCCTTCCGGGCCAGGAGTGC	1770	DB	2791	GGGGGCAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCCGCGCGTTCACC	2850
QY	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560	QY	653	-----	653
DB	1771	GTGGAGAAATGCCAGTACTGTCAGGGGGCTCCCGAGGAGTATGTGAATGCCAGCACTGT	1830	DB	2851	CACCAGATGATGTGTGGAGTATGTGTGATGTGTGGAGCTGATGACTTTTGGGGCC	2910
QY	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580	QY	653	-----	653
DB	1831	TTGCCGTGCCCTCAGTGTGAGCTCAGCCCAAGATGGCTCAGTGACCTGTTTGGACCGGAG	1890	DB	2911	AAACCTTACGATGGGATCCAGCCCGGAGATCCCTGACCTGTGTGAAAAAGGGGAGCGG	2970
QY	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaAlaArgCys	600	QY	653	-----	653
DB	1891	GCTGACCAGTGTGTGGCTGTGGCCCACTATAAGGACCTCCCTCTTCTGGGTGGCCCGCTGC	1950	DB	2971	CTGCCCGAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGTGTCMAATGTTGGATG	3030
QY	601	ProSerGlyValLysProAspLeuSerTyrMetProIleThrLysPheProAspGluGlu	620	QY	653	-----	653
DB	1951	CCGAGCGGTGTGAACCTGACCTCTCTCATGCCCCATCTGGAGTTTCAGATGAGGAG	2010	DB	3031	ATTGACTCTGAATGTCCGGCCAGATTCCGGGAGTGTGTGTCTGAATTTCTCCCGCATGCC	3090
QY	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640	QY	654	-----	654
DB	2011	GGGCGATGCCAGCTTTGGCCCATCACTGACCCACTCTCTGTGTGGACCTGGATGACAAG	2070	DB	3091	AGGGACCCCGAGCGCTTTGTGGTCACTCAGATGAGGACTTGGGCCCGACGCGCTCCCTTG	3150
QY	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	660	QY	665	AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla	684
DB	2071	GGCTGCCCGCCGAGCAGAGAGAGCGCCCTCTGACGTCCATCTCTGTGTGGACCTGGATG	2130	DB	3151	GACAGCACCTTCTACCGCTCACTGCTGAGAGCATGATGAGGAGCTGGTGGATGCT	3210
QY	653	-----	653	QY	685	GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyValGly	704
DB	2131	ATTCTGCTGCTGTGGTCTTTGGGGTGGTCTTTGGGATCTCTATCAAGCGACCGCAGCAG	2190	DB	3211	GAGGAGTATCTGGTACCCCGAGCGGGCTTCTTCTGTCAGACCTGCCCCGGGCGCTGGG	3270
QY	653	-----	653	QY	705	GlyMetValHisIleArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr	724
DB	2191	AAGATCGGAAGTACACGATCGCGAGACTGCTGCAGGAACCGAGCTGGTGGAGCGCGCTG	2250	DB	3271	GGCATGCTCACCAACAGCGCGCTCATCTACACAGGAGTGGCGGTGGGAGCTGACA	3330
QY	653	-----	653	QY	725	LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly	744

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Qy      745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
Db      3391 GCTGGCTCCGATGTATTTGATGGTGACCTGGGAATGGGGGAGCCCAAGGGGCTGCAAGC 3450
Qy      765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
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Qy      785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db      3511 CCTCTGAGACTGATGGCTACGTTGCCCTCCCTGACCTGAGCCCCCAGCCCTGATATGTG 3570
Qy      805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
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Db      3631 CGACCTGCTGGTGCCACTCTGGAAGGGGCCAAGACTCTCTCCCCAGGGAAGATGGGGTC 3690
Qy      845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db      3691 GTCAGAGACGTTTTTGCCCTTTGGGGGTGCCGTGGAGAACCCCGAGTACTTGACACCCAG 3750
Qy      865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
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Qy      885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db      3811 TATTACTGGGACCAAGACCCACAGAGCGGGGGCTCCACCCAGCACCTTCAAGGGACA 3870
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 7, 2004, 08:24:20 ; Search time 124.414 Seconds
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Searched: 682709 seqs, 277475446 residues

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Listing first 45 summaries

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-USER=US09493480 @CEN 1 141 @runat 07062004 082414 5966 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES									
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1	3776	95.5	95.5	3768	2	US-08-625-101-1	Sequence 1, Appli		
2	3776	95.5	95.5	3768	2	US-08-356-786-1	Sequence 1, Appli		
3	3776	95.5	95.5	3768	4	US-09-811-115-2	Sequence 2, Appli		
4	3776	95.5	95.5	4473	2	US-09-048-804-1	Sequence 1, Appli		
5	3776	95.5	95.5	4473	3	US-09-056-105-26	Sequence 26, Appli		
6	3776	95.5	95.5	4473	4	US-09-663-834A-3	Sequence 3, Appli		
7	3776	95.5	95.5	4530	1	US-08-229-515A-9	Sequence 9, Appli		
8	3776	95.5	95.5	4530	1	US-08-645-865-9	Sequence 9, Appli		
9	3776	95.5	95.5	4530	4	US-09-167-322-4	Sequence 4, Appli		
10	3776	95.5	95.5	4530	4	US-09-527-487-1	Sequence 1, Appli		
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16	3471	87.8	1872	3	US-08-422-108-2	Sequence 2, Appli
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19	3205	81.1	3955	1	US-08-645-865-14	Sequence 14, Appli
20	1534	38.8	5532	2	US-08-475-035-3	Sequence 3, Appli
21	1534	38.8	5532	4	US-09-676-610B-17	Sequence 17, Appli
22	1451	36.7	5484	3	US-09-632-580A-3	Sequence 3, Appli
23	1451	36.7	5501	1	US-08-484-438-1	Sequence 1, Appli
24	1451	36.7	5555	1	US-08-484-438-3	Sequence 3, Appli
25	1435	36.3	4905	1	US-07-978-895-3	Sequence 3, Appli
26	1435	36.3	4905	1	US-08-473-119-3	Sequence 3, Appli
27	1435	36.3	4905	2	US-08-475-352-3	Sequence 3, Appli
28	1435	36.3	4905	4	US-09-170-699-3	Sequence 3, Appli
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33	942	23.8	1593	4	US-09-676-610B-25	Sequence 25, Appli
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36	493	12.5	322	1	US-08-421-356-1	Sequence 1, Appli
37	493	12.5	322	4	US-09-046-783-1	Sequence 1, Appli
38	376	9.5	2533	3	US-09-149-922-5	Sequence 5, Appli
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40	369.5	9.3	4723	4	US-09-023-655-1137	Sequence 1137, Ap
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44	323.5	8.2	4975	2	US-08-249-687C-1	Sequence 1, Appli
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ALIGNMENTS

RESULT 1

US-08-625-101-1
; Sequence 1, Application US/08625101
; Patent No. 5869445
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
; TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
; TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
; TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/625,101
; FILING DATE: 01-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:

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RESULT 2

US-08-356-786-1
Sequence 1, Application US/08356786
Patent No. 5877305
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
TITLE OF INVENTION: Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3768 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3768
OTHER INFORMATION: /note= "product = "cerB-b2""
US-08-356-786-1

Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 2 Gaps: 1

US-09-493-480-7 (1-712) x US-08-356-786-1 (1-3768)

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RESULT 3

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US-09-811-115-2
; Sequence 2: Application US/09811115
; Patent No. 6632979
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
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; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT.034A
; CURRENT APPLICATION NUMBER: US/09/811,115
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-811-115-2
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Alignment Scores:

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Pred. No.: 0 Length: 3768
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservatives: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 4 Gaps: 1
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US-09-493-480-7 (1-712) x US-09-811-115-2 (1-3768)

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Db 541 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTTCCGATGTGTANG 600
Qy 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 601 GGTCTCCGCTGCTGGGAGAGAGTTCAGAGATTTGTACAGGCTTACGCGCACTGTCTGT 660
Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
Db 661 GCGGTGGCTGTGCCCGCTGCAGAGGGGCCACTGCGCCACTGACTGTGCTGCATGAGCAGTGT 720
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QY	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260	QY	601	ProSerGlyValLysProAspLeuSerThrMetProIleTrpLysPheProAspGluGlu	620
DB	721	GCTGCCGCTGACGGGCCCCAAGACCTCTGACTGCTGCCCTGCTCCACTTCAACCCAC	780	DB	1801	CCCAGCGTGTGAACCTTGACCTCTCTACATGCCCATCTGGAAAGTTTCCAGATGAGGAG	1860
QY	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrThrAsnThrAspThrPheGlu	280	QY	621	GlyValCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640
DB	781	AGTGGCACTCTGAGCTGCCACCTGGTCACTACACACACACACACGTTTGAG	840	DB	1861	GGCGATGCCAGCTTGGCCCCATCACTGACCCACTCTCTGTGTGGACCTGGATGACAG	1920
QY	281	SerMetProAsnProGluGlyArgThrPheGlyAlaSerCysValThrAlaCysPro	300	QY	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
DB	841	TCCATGCCCAATCCCGAGGGCCGGTATACATTGGGGCCAGCTGTGTGACTGCCCTGTCCC	900	DB	1921	GGCTGCCCGCGCGAGAGAGAGCCAGCCCTCTGACGCTCATCTCTCGCGTGTGGC	1980
QY	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320	QY	653	-----	653
DB	901	TACAACTACTCTTACGGAGCTGGGATCTGCACCCCTGCTGCCCTGCACAAACCAA	960	DB	1981	ATTCTGCTGGTCTGTGGTCTTGGGGTGTGTTTGGGATCCTCATCAAGCGACGGCAGCAG	2040
QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340	QY	653	-----	653
DB	961	GAGGTGACAGCAGAGATGGAAACACAGCGGTGTGAGAGTGCAGCAAGCCCTGTGCCCA	1020	DB	2041	AGATCCCGAAGTACACGATGCGGAGACTGCTGCAGGAAACCGAGCTGTGTGAGCGCGCTG	2100
QY	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360	QY	653	-----	653
DB	1021	GTGTGCTATGGTCTGGGCATGAGACATTGGCAGAGGTGAGGCGAGTTACAGTGCCTAT	1080	DB	2101	ACACCTAGCGGAGCGATGCCAACACAGGCGCAGATGCGGATCCTGAAAGAGACGGAGCTG	2160
QY	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380	QY	653	-----	653
DB	1081	ATCCAGAGTTTGTCTGGCTGCAAGAGATCTTTGGGAGCCTGGCAITTTCTGCCGGAGGC	1140	DB	2161	AGGAAGGTGAAGGTGCTTGGATCTTGGCGCTTTTGGGCACAGTCTACAAAGGSCATCTGGATC	2220
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400	QY	653	-----	653
DB	1141	TTTGTGGGAGCCAGCCTCCAACTGCCGCCCTCCAGCCAGCAGCAGCTTCCAAAGTGT	1200	DB	2221	CCTGATGGGAGNAATGTGAATTTCCAGTGGCCATCAAAGTGTGAGGGAAACACATCC	2280
QY	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	420	QY	653	-----	653
DB	1201	GAGACTCTGAGAGATCAGGTTTACCTATATCTCTCAGCATGGCCGCGAGACGCTTGCCT	1260	DB	2281	CCCAAGCCCAACAAAGAAATCTTAGACGAAGCATACGTGTATGCTGTGTGGTCTCCCA	2340
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440	QY	653	-----	653
DB	1261	GACCTCAGGTCTTCCAGAACTGCAAGTAATCCGGGACGAATTTCTGCACAAATGCGCC	1320	DB	2341	TATGTCTCCGCTTCTGGGCATCTGCTGACATCCACCGTGCAGCTGTGTGACACACATT	2400
QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460	QY	653	-----	653
DB	1321	TACTGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGGCTCACTGAGGGAA	1380	DB	2401	ATGCCCTATGGCTGCTCTTAGACCATGTCCGGGAAACCGCGGACGCTGGCTCCCG	2460
QY	461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480	QY	653	-----	653
DB	1381	CTGGGCAGTGGACTGGCTCATCCACCATAACACCCACCTCTGCTTGTGTGCAACGGTG	1440	DB	2461	GACCTGTGAACTGTGTATGACAGATTGCCAAGGGATGAGCTACTTGGAGGATGTGCGG	2520
QY	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500	QY	653	-----	653
DB	1441	CCCTGGGACCAAGCTCTTTCGGAACCCGACCAAGCTCTGCTCCACACTGCGCAACCGCCA	1500	DB	2521	CTCGTACACAGGAGCTTGGCCGCTCGGAACGTGCTGTGTCAAGAGTCCCNACCATGTCAA	2580
QY	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520	QY	653	-----	653
DB	1501	GAGGACAGTGTGTGGCGAGGGCTGGCTGCCACCGAGCTGTGCGCCCGAGGGCACTGC	1560	DB	2581	ATTACAGACTTGGGGTGGCTCGGCTGTGACATTTGACGACGACAGAGTACCATGSCAGAT	2640
QY	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540	QY	653	-----	653
DB	1561	TGGGGTCCAGGGCCACCCAGTGTGTCACTGACGACGATTTCTTGGGGCCAGGAGTGC	1620	DB	2641	GGGGGCAAGGTGCCATCAAGTGGATGGCGCTGGAGTTCATTTCTCCCGCGCGGTTCACC	2700
QY	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560	QY	653	-----	653
DB	1621	GTGGAGGAATGCCAGTACTGACGGGCTCCCGAGGGAGTATGTGAATGCCAGGCACTGT	1680	DB	2701	CACAGAGTGTGTGGAGTTATGTGTGACTGTGTGTGGGAGTGTGACTTTTGGGGCC	2760
QY	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580	QY	653	-----	653
DB	1681	TTGCGGTGCCACCTTGAGTGTCAAGCCCGAGAGTGGCTCAGTGCCTGTGTGGACCGGAG	1740	DB	2761	AAACCTTACATGGGATCCCGAGCCCGGAGATCCCTGACCTGCTGGAAGGGGAGCGG	2820
QY	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys	600	QY	653	-----	653
DB	1741	GCTGACAGTGTGTGGCTGTGGCCACTATAAGGACCTCCCTCTCTCGGTGGCCCGCTGC	1800	DB	2821	CTGCCCGAGCCCGCATCTGCACCATTTGATGTCTACATGATCATGTGTCAAATGTTGGATG	2880
QY				QY	653	-----	653

Db 2881 ATTGACTCTGAATGTCGGCCCAAGATTTCGGGAGTTGTGTCTGTAATTCCTCCGCGATGGCC 2940
Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGGACCCCGAGCGCTTTGTGTGTCATCCAGAAATGAGGACTTGGGCGCCAGCGATCCCTTG 3000
Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGCACCTTCTACCGCTCATCTGCTGGAGACCATGATGATGGGGGACCTGGTGGATGCT 3060
Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyValGly 704
Db 3061 GAGGAGATATCTGGTACCCAGAGGCTTCTTCTGTCCAGACCTTCCCTCCCGGCGCTGG 3120
Qy 705 GlyMetValHisHisArgHisArg 712
Db 3121 GGCATGTTCCACACAGGCACCGC 3144

RESULT 4

US-09-048-804-1
; Sequence 1, Application US/09048804
; Patent No. 5968748
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett, Allan Lipton, Lois M. Witters
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF
; TITLE OF INVENTION: HUMAN HER-2 EXPRESSION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5968748rls LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103

COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/048,804
; FILING DATE: Herewith

CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-2913
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4473 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Unknown
; ANTI-SENSE: No

US-09-048-804-1

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 2 Gaps: 1

US-09-493-480-7 (1-712) x US-09-048-804-1 (1-4473)

Qy 1 MetGluLeuAlaAalaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProGlyVala 20
Db 175 ATGGAGCTGGCGGCTTGTGCGCTTGTGCGGCTTCTTCTCGCCCTTCTTGGCCCGCGAGCC 234

Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetIysLeuValArgLeuProAlaSerProGlu 40
Db 235 GCGAGCACCCCAAGTGTGCACCGGCACAGACATGAAGCTCGCGCTCCCTGCCAGTCCGAG 294
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 295 ACCACCTGGACATGCTCCGCCACCTCTACAGGGCTGCCAGTGGTGGCAGGAACCTG 354
Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 355 GAACCTCACCTACCTGCCACCAATGCCAGCCTGTCTTCTTCGAGGATATCCAGGAGGTG 414
Qy 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 415 CAGGGCTAGCTGCTCATCGCTCACCAACCAAGTGGCAGGTCCTCCACTGCAGAGGCTGCCG 474
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 475 ATTGTGCGAGGACCCAGCTCTTTGAGGACCACTATGCTGCGCTGGCTGTAGCAATGGA 534
Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
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Qy 141 GlnLeuArgSerLeuThrGluIleLeuIysGlyValLeuIleGlnArgAsnProGln 160
Db 595 CAGCTTCGAAGCCTCACAGAGATCTTGAAGAGAGGGTCTTGATCCAGCGGAACCCCGAG 654
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Db 655 CTCTGCTACCGAGGACCAAGATTTGTGAAGGACATCTTCCACAGAACCAACAGCTGGCT 714
Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 715 CTCACACTGATAGACACCAACCGCTCTCGGGCTCGCCACCCCTGTTCTCCGATGTGAAG 774
Qy 201 GlySerArgCysTrpGlyLeuSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
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Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
Db 835 GCCGGTGGCTGTGCCCGCTGCAAGGGGCCACTGCCCACTGACTGCTGCCATGAGCAGTGT 894
Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 895 GCTGCCGCTGCAAGGGGCCCCAAGCACCTCTGACTGCTGGCTGCCCTCCACTTCAACCCAC 954
Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 955 AGTGGCATCTGTGAGCTGCACCTGCCCGCCAGCCCTGAGTACCTACCAACACAGACAGTTGAG 1014
Qy 281 SerMetProAsnProGluValArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 1015 TCCATGCCCAATCCCGAGGGCCGGTATACATTTGGCGCCAGCTGTGTGACTGTGTCCC 1074
Qy 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db 1075 TACAACTACCTTTCTACGGAGCTGGGATCTCGCACCTCTGCTGCCCTCCGCAACACCA 1134
Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
Db 1135 GAGGTGCACAGCAGAGATGGAAACAGCGGTGTGTGAAGTGCAGAGAGGCTCTGTGCCCGA 1194
Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
Db 1195 GTGTGCTATGTGTCTGGGCATGGAGCATTGCGAGAGGTGAGGGCACTTACCAGTGCCAAT 1254
Qy 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 1255 ATCCAGGAGTTTGTCTGGCTGCAAGAAGATCTTTGGGAGCTTGGCAATTTCTGCGCGAGAGC 1314

Qy	381	Phe	Asp	Gly	Asp	Pro	Ala	Ser	Asn	Thr	Ala	Pro	Leu	Gln	Pro	Glu	Gln	Leu	Gln	Val	Phe	400
Db		TTT	GAT	GGG	ACC	CAG	CTC	CAA	CAC	TGC	CCG	CTC	CAG	CCG	CAG	CAG	CAG	CAG	CTC	CAG	TGT	1374
Qy	401	Glu	Thr	Leu	Glu	Ile	Thr	Gly	Tyr	Leu	Tyr	Ile	Ser	Ala	Trp	Pro	Asp	Ser	Leu	Pro	420	
Db		GAG	ACT	CTG	AAG	AGAT	AC	AGG	TTA	CCT	TAT	TAC	ATC	TCT	CAG	ATG	CGC	CGG	AC	AGC	TGC	1434
Qy	421	Asp	Leu	Ser	Val	Phe	Gln	Asn	Leu	Gln	Val	Ile	Arg	Gly	Arg	Ile	Leu	His	Asn	Gly	Vala	440
Db		GAC	CT	CAG	CGT	CTT	CC	AGA	ACC	TGC	AGT	ATA	CCG	G	GAG	CGA	ATT	CTG	CA	CA	AT	1494
Qy	441	Tyr	Ser	Leu	Thr	Leu	Gln	Gly	Leu	Gly	Ile	Ser	Trp	Leu	Gly	Leu	Arg	Ser	Leu	Arg	Glu	460
Db		TAC	T	CGT	CGA	CCCT	GC	AAG	G	G	G	C	T	G	G	C	T	C	A	C	T	1554
Qy	461	Leu	Gly	Ser	Gly	Leu	Ala	Leu	Ile	His	His	Asn	Thr	His	Ser	Cys	Phe	Val	His	Thr	Val	480
Db		CTG	G	CAG	T	G	A	C	T	G	G	C	C	T	A	T	C	A	C	A	C	1614
Qy	481	Pro	Trp	Asp	Gln	Leu	Phe	Arg	Asn	Pro	His	Gln	Ala	Leu	Leu	His	Thr	Ala	Asn	Arg	Pro	500
Db		CCC	T	G	G	A	C	CA	G	CT	CTT	T	T	G	G	A	C	CC	CA	C	T	1674
Qy	501	Glu	Asp	Glu	Cys	Val	Gly	Glu	Gly	Leu	Ala	Cys	His	Gln	Leu	Cys	Ala	Arg	Gly	His	Cys	520
Db		GAG	CA	CAG	TGT	GTG	G	G	G	G	G	C	CT	G	C	CA	C	CA	C	AG	TGC	1734
Qy	521	Trp	Gly	Pro	Gly	Pro	Thr	Gln	Cys	Val	Asn	Cys	Ser	Gln	Phe	Leu	Arg	Gly	Gln	Glu	Cys	540
Db		TGG	G	G	T	CC	A	G	G	CC	C	CA	C	CA	G	T	CT	T	CC	CA	C	1794
Qy	541	Val	Glu	Glu	Cys	Arg	Val	Leu	Gln	Gln	Gly	Leu	Pro	Arg	Glu	Tyr	Val	Asn	Ala	Arg	His	560
Db		GTG	A	G	A	AT	CC	CA	G	T	ACT	GC	A	G	G	G	T	AT	G	AT	G	1854
Qy	561	Leu	Pro	Cys	His	Pro	Glu	Cys	Gln	Pro	Gln	Asn	Gly	Ser	Val	Thr	Cys	Phe	Gly	Pro	Glu	580
Db		TTG	CG	T	GC	CA	CC	CT	G	AG	T	GC	CC	CA	GA	AT	T	GC	CT	CT	T	1914
Qy	581	Ala	Asp	Gln	Cys	Val	Ala	Cys	Ala	His	Tyr	Ile	Asp	Pro	Phe	Cys	Val	Ala	Arg	Cys	600	
Db		GCT	GA	CC	CA	G	T	GT	G	GG	CC	CT	G	T	AT	A	A	G	A	C	C	1974
Qy	601	Pro	Ser	Gly	Val	Lys	Pro	Asp	Leu	Ser	Tyr	Met	Pro	Ile	Trp	Lys	Phe	Pro	Asp	Glu	Glu	620
Db		CCC	A	G	CG	T	G	T	GA	A	AC	CT	CT	CT	CA	T	AT	G	AT	G	AT	2034
Qy	621	Gly	Ala	Cys	Gln	Pro	Cys	Pro	Ile	Asn	Cys	Thr	His	Ser	Cys	Val	Asp	Leu	Asp	Asp	Lys	640
Db		GGC	GA	T	CC	CA	CC	CT	T	G	CC	CA	C	CA	C	CA	C	CA	C	CA	C	2094
Qy	641	Gly	Cys	Pro	Ala	Glu	Gln	Arg	Ala	Ser	Pro	Leu	Thr	Ser	-----	-----	-----	-----	-----	-----	653	
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2455	DB	CCCAAGCCCAACAAAGAAATCTTTAGACGAAGCATACGTGATGGCTGGTGTGGCTCCCCCA	2514
653	QY	-----	653
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2575	DB	ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAACCGCGAAGCGCTGGCTCCAG	2634
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2635	DB	GACCTGCTGAACCTGGTGTATGCAGATTGCCAAGGGATGAGCTACCTGGAGGATGTGCGG	2694
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653	QY	-----	653
2815	DB	GGGGCAAGGTGCCCATCAAAGTGGATGGCGCTGGAGTCCATTCTCCGCGCGGTTCAAC	2874
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2875	DB	CACCAGAGTGAATGTGTGAGTTATAGTGTGACTGTGTGGAGCTGATGAATTTTGGGGCC	2934
653	QY	-----	653
2935	DB	AAACCTTACGATGGGATCCGAGCCCGGAGATCCCTGACCTGTGGAAAGGGGAGCGG	2994
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2995	DB	CTGCCCCAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGTCTCAAAATGTTGGATG	3054
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3055	DB	ATTGACTCTGAATGTGCGGCCAAGATTCCGGAGTGTGTCTGAATTTCTCCCGATGGCC	3114
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3115	DB	AGGACCCCCAGCGCTTTTGGTCAATCCAGATGAGGACTTGGSCCAGCCAGTCCCTTG	3174
665	QY	AspSerThrPheTyrArgSerLeuLeuGluAeAspAspMetGlyAspLeuValAspAla	684
3175	DB	GACAGCACCTTCTACTCCGCTCACTCTCTGGAGCAGATGACATGGGGGACCTGGTGGATGCT	3234
685	QY	GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyValaGly	704
3235	DB	GAGGAGTATCTGGTATCCCAAGAGGGCTTCTTCTGTCCAGACCCTTGCCCCGGGCGCTGGG	3294
705	QY	GlyMetValHisHisArgHisArg	712
3295	DB	GGCATGTGTCACCCAGGCCACCGC	3318

RESULT 5
US-09-056-105-26
; Sequence 26, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
; APPLICANT: KIPPS, THOMAS J.
; APPLICANT: WU, YUNQI
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
; TITLE OF INVENTION: PROCESSING
; FILE REFERENCE: 233/221

141 GlnLeuArgSerLeuThrGluIleLeuLeuLysGlyValLeuLeuLeuGlnArgAsnProGln 160
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595 CAGCTTCGAAGCCTCAGAGATCTTTGAAAGGAGGGGTCTTGATCCAGCGGAAACCCCGAG 654
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655 CTCCTGTACAGGACACGATTTTGTGGAAGGACATCTTCACAAAGAAACAAACGAGCTGGCT 714
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401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420
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1375 GAGACTCGAAGAGATCAGAGTTACTCTATACATCTCAGCATGGCCGCGAGCTGCTGCT 1434
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Qy	665	AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla	684
Db	3175	GACAGCACCTTCTACCGCTCACTCTGTGGAGGACGATGACATGGGGGACCTGTGTGGATGCT	3234
Qy	685	GluGlnTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyValaGly	704
Db	3235	GAGGAGTATCTGTATACCCAGCAGGGGTCTTCTGTCCAGACCCCTGCCCCGGGCGCTGGG	3294
Qy	705	GlyMetValHisHisArgHisArg	712
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RESULT 7

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US-08-229-515A-9
; Sequence 9, Application US/08229515A
; Patent No. 5518885
; GENERAL INFORMATION:
; APPLICANT: RAZIUDDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPlastic DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/229,515A
; FILING DATE: 19 APR 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414,608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 9:

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2671 CTCGTACACAGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 2730
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RESULT 9

US-09-167-322-4

; Sequence 4, Application US/09167322

; Patent No. 6365151

; GENERAL INFORMATION:

; APPLICANT: Allergeny University of the Health

; Sciences, Halpern, Michael S.

; England, James M.

; TITLE OF INVENTION: CANCER VACCINE

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.

; STREET: Suite 1800, Two Penn Center Plaza

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

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1831	TTGCCGTGCCACCCCTGAGTGTTCAGCCCCAGAAATGGCTCAGTGCCTCTTTTGACCGGAG		1890
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1891	GCTGACCAGTGTGTGGCTGTGGCCACTATAAGAGACCTCCCTTTCTGCGTGGCCCGCTGC		1950
601	ProSerGlyValLysProAspLeuSerTyrMetProIleTTrpLysPheProAspGluGlu		620
1951	CCCGAGCGGTGAACCTGCACCTCTCTCTACATGTCCTCATCTGGAAAGTTTCCAGATGAGAG		2010
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2191	AAGATCCGGAAGTACACGATCGGAGACTGCTGCAGGAAACGGAGCTGTGTGGAGCCGCTG		2250
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2851	CACCAGATGATGTGGAGTTATGTGTGTGACTGTGTGGGAGCTGTATGACTTTTGGGGCC		2910

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Qy	654	-----GlnAsnGluAspLeuGlyProAlaSerProLeu	664
Db	3091	AGGGACCCCCCAGCGCTTTTGTGGTCATCCAGAAATGAGACTTGGGCCCAGACGACGCTCCCTTG	3150
Qy	665	AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla	684
Db	3151	GACAGCACCTTCTACCGCTCACTGCTGGAGGAGATGACATGGGGGACCTGTGTGGATGCT	3210
Qy	685	GluGlnTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly	704
Db	3211	GAGGATATCTGGTACCCAGCAGGCGTCTTCTGTCCAGACCTCGCCCCGGGCGCTGGG	3270
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RESULT 10

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US-09-527-487-1
? Sequence 1, Application US/09527487
? Patent No. 6528060
? GENERAL INFORMATION:
? APPLICANT: Nicolette, Charles
? TITLE OF INVENTION: HER2 ANTIGENIC PEPTIDES
? FILE REFERENCE: 126881309200
? CURRENT APPLICATION NUMBER: US/09/527,487
? CURRENT FILING DATE: 2000-03-16
? NUMBER OF SEQ ID NOS: 9
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO 1
? LENGTH: 4530
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (151)..(3915)
US-09-527-487-1

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Alignment Scores:					
Pred. No.:	0	Length:	0	Matches:	4530
Score:	3776.00			Conservative:	712
Percent Similarity:	67.94%			Mismatches:	0
Best Local Similarity:	67.94%			Indels:	336
Query Match:	95.50%			Gaps:	1
DB:	4				

US-09-493-480-7 (1-712) x US-09-527-487-1 (1-4530)

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Db	211	GCGAGCACCCAAAGTGTGCACCGGCACAGACATGAAGCTCGCGCTCCCTGCCAGTCCCGAG	270	
Qy	41	ThrHisLeuAspMetLeuArgGHisLeuTrpGlnGlyCysGlnValValGlnGlyAsnLeu	60	
Db	271	ACCACCTGGACATGCTCCGCCACCTCTTACCAGGGCTGCCAGGTGTGTCAGGGAAACCTTG	330	
Qy	61	GluLeuThrTrpLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal	80	

331	Db	 GAACTCACCTACCTGCCCAACAAATGCCAGCCTCTCTCTCTCTGTCAGATATCCAGGAGGTG	390
81	Qy	 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100
391	Db	 CAGGGCTACGTGCTCATCTGCTCAACAACAGTGAAGGAGGTCTCCACTGCAGAGGCTGCCG	450
101	Qy	 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120
451	Db	 ATTGTGCGAGGCACCCAGCTCTTTGAGSACAACTATGCCCTTGGCCGTGTGTAGACAATGGA	510
121	Qy	 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140
511	Db	 GACCGCTGAACAATACACCCCTGTTCACAGGGCCCTCCCCAGAGGAGCCCTGCCGGAGCTG	570
141	Qy	 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln	160
571	Db	 CAGCTTTCGAAGCCCTACAGAGATCTTGAAAGGAGGGGTCTTGATCCAGCGGAACCCCCAG	630
161	Qy	 LeuCysTyrGlnAspThrIleLeuTyrPheAspIlePheHisAsnAsnGlnLeuAla	180
631	Db	 CTCTGCTACCAAGGACACGATTTTGTGAAGSACATCTTCCACAAGAACCAACAGCTGGCT	690
181	Qy	 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
691	Db	 CTCACACTGATAGACACCAACCGCTCTCGGGCCCTGCCACCCCTGTTCTCCGATGTGTAAAG	750
201	Qy	 GlySerArgCysTyrGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220
751	Db	 GGCTCCCGCTGCTGGGAGAGAGTTCTGAGAGATTTGTAGAGCCCTGACGGGACTGTCTGT	810
221	Qy	 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	240
811	Db	 GCCGGTGGCTGTGCCCTGTGAAGGGGCCACTGCCCCACTGACTCTCTGCCATGAGCAGTGT	870
241	Qy	 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
871	Db	 GCTGCCGGCTGCACGGGCCCAACAGCACTCTGACTGCTCTGGCTGCCCTCCACTTCAACAC	930
261	Qy	 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280
931	Db	 AGTGGCATCTGTGAGCTGCATCTGCCAGCCCTGGTCACTTACAACACAGACACGTTTGAG	990
281	Qy	 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300
991	Db	 TCCATGCCCAATCCCGAGGGCCGGTATACATTGGGGCCAGCTGTGTGACTGCTCTGCC	1050
301	Qy	 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
1051	Db	 TACAACACTACCTTTACGGACGTGGGATCTCTGCACCCCTGCTGTCTGCCCTCTGCACACAA	1110
321	Qy	 GluValThrAlaGluAspGlyThrClnArgCysGluLysCysSerLysProCysAlaArg	340
1111	Db	 GAGGTGACAGCAGAGAGATGGAACACAGCGGTGTGAGAAGTGCAGAGGCCCTGTGCCCGGA	1170
341	Qy	 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
1171	Db	 GTGTGCTATGTCTGGGCATGAGGACCTTGGAGAGGTGAGGGCAGTTACCATGTGCCAAT	1230
361	Qy	 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380
1231	Db	 ATCCAGGAGTTTGTCTGCTGCCAAGAAGATCTTTTGGAGCCCTGGCAATTTCTGCCGAGAGC	1290
381	Qy	 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGluValPhe	400
1291	Db	 TTTGTATGGGGACCCAGCCCTCCAACATCTCCCGCTTCCAGCCAGAGCAGCTCCAAGTGT	1350
401	Qy	 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro	420
1351	Db	 GAGACTCTGGAAGAGATCACAGTTACTCTATACATCTCAGGATTTGGCCGGAACAGCTGCT	1410
421	Qy	 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440

1411	DB	GACCTCAGCGTCTTCAGAACCTCGCAGTAATCCGGGGACGAATTCGTGCACATGATGGCGCC	1470
441	QY	TyrSerLeuThrLeuGlnGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
1471	DB	TACTCGCTGACCTCTGCAGGGCTGGGCATCAGCTGCCTGGGGCTGGCTCACTGAGGGAA	1530
461	QY	LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal	480
1531	DB	CTGGGCAGTGGACTGGGCCCTCATCCACCATTAACCCACCTCTGCTTGGTGCACACGGTG	1590
481	QY	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
1591	DB	CCCTGGGACACGCTCTTTTGGGACCCCGCACCAAGCTCTGCTCCACACTGCCAACCGGCCA	1650
501	QY	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
1651	DB	GAGCAGAGTGTGTGGCGAGGGCTGGCCCTGCACCCAGCTGTGGCGCCGAGGGCACTGC	1710
521	QY	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
1711	DB	TGGGCTCCAGGGCCACCCAGTGTGTCACTCGAGCCAGTCTCTTGGGGCCAGGAGTGC	1770
541	QY	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTrpValAsnAlaArgHisCys	560
1771	DB	GTGGAGGATGCCAGTACTTCGAGGGGCTCCCCAGGGAGTATGTGAATGCAGGCACCTGT	1830
561	QY	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
1831	DB	TTCGGTGCACCCCTGAGTGTTCAGCCCCAGATGGCTCAGTGACTCTTTTGGACCGGAG	1890
581	QY	AlaAspGlnCysValAlaCysAlaHisTrpIlyAspProProPheCysValAlaArgCys	600
1891	DB	GCTGACCACTGTGTGGCTGTGTGCCACTATAGAAGACCTCCCTTCTCGGTGGCCCGCTGC	1950
601	QY	ProSerGlyValIlyProAspLeuSerTrpMetProIleTrpIlyPheProAspGluGlu	620
1951	DB	CCCAGCGTGTGAACCTTGACCTCTCTACATGCCCTCTGATGGACCTCTGGATGACAAG	2010
621	QY	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspIys	640
2011	DB	GGCGCATGCCGCTTGCCCATCAACTGCACCCACTCTGTGTGGACCTCTGGATGACAAG	2070
641	QY	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
2071	DB	GGCTGCCCGCGAGCAGAGAGCCAGCCCTCTGACGCTCATCGCTCTCGGGTGGTGGC	2130
653	QY	-----	653
2131	DB	ATTCTGCTGGTGTGGTCTTGGGGTGGTCTTTGGGATCTCATCAAGCAGCGCAGCAG	2190
653	QY	-----	653
2191	DB	AAGATCCGGAAGTACACGATGCGGAGACTGTCTGCAGGAAACGGAGCTGTGGAGCCGCTG	2250
653	QY	-----	653
2251	DB	ACACCTAGCGGAGCGATGCCCAACGCGCAGATGCGGATCTCTGAAGAGACGGAGCTG	2310
653	QY	-----	653
2311	DB	AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACTCTTACAGGGCATCTGGATC	2370
653	QY	-----	653
2371	DB	CTGTATGGGGAGATGTGAAAATTCAGTGGCCATCAAAGTGTGTGAGGGAACACATCC	2430
653	QY	-----	653
2431	DB	CCCAAGGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGTGTGGGTCCCCA	2490
653	QY	-----	653
2491	DB	TATGTCTCCGCGCTTCTGGGCAATCTGCCCTGACATCCAGGTGCGAGCTGTGTGACACAGCTT	2550

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QY 653 ----- 653
Db 2551 ATGCGCTATGGCTGCTCTTAGACCATGTCGGGAAACCGGACGCTGGGCTCCAG 2610
QY 653 ----- 653
Db 2611 GACCTGCTGAACCTGGTGTATGTCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGGG 2670
QY 653 ----- 653
Db 2671 CTGCTACACAGGACTTGGCGCTCGGAACGTGCTGCTCAAGAGTCCCAACCATGTCAA 2730
QY 653 ----- 653
Db 2731 ATTACAGACTTGGGGCTGGCTCGGCTGCTGTCGACATTGACGAGACAGAGTACCATGCAGAT 2790
QY 653 ----- 653
Db 2791 GGGGGCAAGGTGCCCATCAAGTGTGATGGCTGGAGTCCATTCTCCCGCGCGGTTTCA 2850
QY 653 ----- 653
Db 2851 CACCAGAGTGTATGTCGAGTTATGGTGTGACTGTGTGGGAGCTGATGACTTTTGGGCGCC 2910
QY 653 ----- 653
Db 2911 AAACCTTACGATGGGATCCAGCCCGGAGATCCCTGACCTGTGGAAAGGGGAGCGG 2970
QY 653 ----- 653
Db 2971 CTGCCCCAGCCCCCATCTGCAACATTGATGTCTACATGATCATGGTCAAAATGTTGGATG 3030
QY 653 ----- 653
Db 3031 ATTGACTCTGAATGTCGGCAAGATTCGGGAGTTGGTGTCTGAATTTCTCCGCGATGGCC 3090
QY 654 ----- GluAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3091 AGGGACCCCGAGCGCTTTGTGTCTATCCAGAAATGAGGACTTGGGCGCCAGCGCTCCCTTG 3150
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3151 GACGACCTCTTACCCCTACTCTGAGAGCAGCATGACATGGGGAGCCTGGTGGATGCT 3210
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3211 GAGGAGTATCTGTTACCCAGCAGCGCTTCTTCTGTCCAGACCTTGCCCCGGGCGCTGGG 3270
QY 705 GlyMetValHisArgHisArg 712
Db 3271 GGCATGGTCCACCACAGGCGACGCG 3294
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RESULT 11

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US-09-877-177A-11
; Sequence 11, Application US/09877177A
; Patent No. 6582919
; GENERAL INFORMATION:
; APPLICANT: K. Danenberg
; TITLE OF INVENTION: Method of determining Epidermal Growth
; TITLE OF INVENTION: Factor Receptor and HER2-Neu Gene Expression
; TITLE OF INVENTION: and Correlation of Levels Thereof With Survival
; FILE REFERENCE: 11220/120
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-877-177A-11
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Alignment Scores:
Pred. No.: 0 Length: 4530
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
Db: 4 Gaps: 1
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US-09-493-480-7 (1-712) x US-09-877-177A-11 (1-4530)

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QY 1 MetGluLeuAlaLeuCysArgTProGlyLeuLeuLeuAlaLeuLeuProProGlyAla 20
Db 151 ATGAGAGTGGGGGCTTGTGGCGCTGGGGGCTCTCTCTGGCCCTCTTGGCCCCCGGAGCC 210
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 211 GCGAGCACCCCAAGTGTGCACCGGCACACATGAAGCTGGCGCTCCCTGCGAGTCCCGAG 270
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyLeu 60
Db 271 ACCCAGCTGGACATGCTCCGCCACCTCTACAGGGCTGCCAGGTGGTGCAGGGAACCTG 330
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 331 GAATCTACCTACCTGCCCAATGCCAGCTGTCTCTCTGCGAGATATCCAGGAGGTG 390
QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 391 CAGGGCTACGCTGCTCATCGCTCACACCAAGTGAAGGAGGTCCCACTGCAGAGGTGCGG 450
QY 101 IleValArgGlyThrGlnLeuPheGluAspSerTyrAlaLeuAlaValLeuAspGlnGly 120
Db 451 ATTGTGGAGGACACCCAGCTCTTTGAGGACAACTATGCCCCCTGGCCGCTGACAAATGA 510
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 511 GACCCGCTGACACATACCAACCCCTGTACAGGGGCTCTCCAGGAGGCTGGCGGAGCTG 570
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 571 CAGCTTCGAGCCTCACAGAGATCTTGAAGAGGGGTCTTGATCCAGCGGAAACCCCGAG 630
QY 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnGlnLeuAla 180
Db 631 CTCTGCTACCAAGGACACGATTTTGTGAAGAGACATCTTCCACAGAAACAACCGCTGGCT 690
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 691 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTTCTCCGATGTGTAG 750
QY 201 GlySerArgCysTyrGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 751 GCGTCCGCTGCTGGGAGAGAGATTCTGAGGATTTGTACAGAGCTGCACGCGACTGTCTGT 810
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
Db 811 GCCGCTGCTGTGCCCGCTGACAGGGCCACTGCCCACTGCTGCTCCATGACAGAGTGT 870
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 871 GCTCCCGGCTGACCGGGCCCCAAGCACTCTGACTGCCCTGGCTGGCTCCACTTCAACAC 930
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 931 AGTGGCATCTGTGAGCTGCACTGCCAGCCCTGGTCACTTACACACAGACACGTTTGG 990
QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 991 TCCATGCCCAATCCCGAGGGCGGTATACATTTGGCGCGCAGCTGTGTGACTGCTGTCTCC 1050
QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db 1051 TACAACTACCTTTCTACGAGAGTGGGATCTTGCACCCCTCGTCTGCCCCCTGCACACCAA 1110
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QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340	QY	653	-----	653
DB	1111	GAGGTGACAGCAGAGATGGAAACACAGCGGTGTGAGAGTGCAGCAAGCCCTGTGCCGA	1170	DB	2191	AAGATCCGGAGACTACAGATGCGAGACTGCTGCAGGAAACGGAGCTGTGTGAGCCGCTG	2250
QY	341	ValCysTyrGlyLeuGluMetGluHisLeuArgGluValArgAlaValThrSerAlaLen	360	QY	653	-----	653
DB	1171	GTGTCTATGTCTGGCATGAGACATTCGCGAGAGGTGAGGCGAGTTACCAAGTGCCAT	1230	DB	2251	ACACCTAGCGGAGCGATGCCAAACAGCGCGAGATGCGGATCCTGAAAGAGACGGAGCTG	2310
QY	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380	QY	653	-----	653
DB	1231	ATCCAGGAGTTGTCTGGCTGCAAGAAGATCTTTGGGAGCTTGCCATTTCTGCGCGAGAGC	1290	DB	2311	AGGAAGGTGAAGTGTCTGGATCTGCGCTTTTGGGCACAGTCTTACAAGGGCATCTGGATC	2370
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400	QY	653	-----	653
DB	1291	TTTGTATGGGAGCCAGCTCCAACTGCCCCGCTCCAGCCAGAGCAGCTCCAAGTGT	1350	DB	2371	CTGTATGGGAGAAATGTGAAATTTCCAGTGGCCATCAAAGTGTGAGGGGAAACACATCC	2430
QY	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro	420	QY	653	-----	653
DB	1351	GAGACTCTGGAAGAGATCACAGTTTACCTATACATCTCAGCATGGCCGACAGCTGCT	1410	DB	2431	CCCAAGCCCAACAAAGNAATCTTAGACGAAGCATACGTGATGCTGTGTGGCTCCCCA	2490
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440	QY	653	-----	653
DB	1411	GACCTCAGCGTCTTCAGAACTGCAAGTAATCCGGGAGGAATTCGCAATGGCGCC	1470	DB	2491	TATGTCTCCCGCTTCTGGGCATCTGCCTGACATCCACCGTGCAGCTGTGTGACACAGCTT	2550
QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuGlyLeuArgSerLeuArgGlu	460	QY	653	-----	653
DB	1471	TACTCGCTGACCCCTGCAGAGGCTGGGCATCAGCTGCTGGGCTGGCGCTCACTGAGGGA	1530	DB	2551	ATGCCCTATGGCTGCTCTTAGACCATGTCCGGGAAAAACGGCGGACGCTGGGCTCCAG	2610
QY	461	LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal	480	QY	653	-----	653
DB	1531	CTGGGAGTGGAGTGGCCCTCATCACCAATACACCCACTCTGCTTCTGTGACACGGTG	1590	DB	2611	GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG	2670
QY	481	ProTyrAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500	QY	653	-----	653
DB	1591	CCCTGGGACCACTCTTTGGAAACCGCACCAAGCTCTGCTCCACACTGCCAACCGGCCA	1650	DB	2671	CTCGTACACAGGACTTGGCCGCTCGGAACTGTCTGGTCAAAGAGTCCCAACCATGTCAA	2730
QY	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuLeuAsnArgGlyHisCys	520	QY	653	-----	653
DB	1651	GAGGACGAGTGTGTGGCGAGGCGCTGGCTGCCACCACTGTGGCGCCGAGGGCACTGC	1710	DB	2731	ATTACAGACTTCGGGCTGGCTCGGCTGTGGACATTGACGAGACAGAGTACCATGCAGAT	2790
QY	521	TyrGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540	QY	653	-----	653
DB	1711	TGGGTTCACAGGCCACCCAGTGTGTCAACTGACGACAGTCTCTTCGGGGCCAGGATGC	1770	DB	2791	GGGGCCAGGTGCCCCATCAAGTGGATGGCGCTGAGTGCATTCTCCCGCGCGGTTCCAC	2850
QY	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560	QY	653	-----	653
DB	1771	GTGGAGGATGCGAGTACTGACGAGGCTCCCGAGGAGTATGTGAATGCCAGGCACTGT	1830	DB	2851	CACACAGAGTGTGTGGAGTTATGTGTGACTGTGTGTGGAGCTGATGACTTTTGGGGCC	2910
QY	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580	QY	653	-----	653
DB	1831	TTGCCGTGCCACCTGAGTGTGAGCCCGCAAGATGGCTGAGTGAACCTTTTGGACCGGAG	1890	DB	2911	AAACCTTACGATGGGATCCAGCCCGGAGATCCCTGACCTGTGCGGAGGAGCGG	2970
QY	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys	600	QY	653	-----	653
DB	1891	GCTGACAGTGTGGCTGTGCCCACTATAGGACCTCCCTCTGCGTGGCCCGCTGC	1950	DB	2971	CTGCCCGACCCCGCCATCTGCACCAATTGATGTCTACATGATCATGTGTCAAATGTTGATG	3030
QY	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu	620	QY	653	-----	653
DB	1951	CCGAGCGGTGAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG	2010	DB	3031	ATTGACTCTGAATGTGCGCAAGATTCGGGAGTTGGTGTCTGAAATCTCCCGCATGGCC	3090
QY	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640	QY	654	-----	664
DB	2011	GGCGCATGCGAGCTTGGCCCATCAACTGCACCCACTCTGTGTGGACCTTGGATGACAAG	2070	DB	3091	AGGGACCCCGCGCTTTGTGGTTCATCCAGATGAGGACTTGGGCCCGCCAGTCCCTTG	3150
QY	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer-----	653	DB	665	AspSerThrPheTyrArgSerLeuLeuAspAspAspMetGlyAspLeuValAspAla	684
DB	2071	GGTGTCCCCCGAGCAGAGAGCCAGCCCTCTGACGTCCATCGTCTCTGGGTGGTGGC	2130	DB	3151	GACAGCACCTTCTACCGCTCACTGTCTGGAGGACGATGACATGGGGGACCTTGGTGGATGT	3210
QY	653	-----	653	DB	685	GluGluTyrLeuValProGlnGlyPhePheCysProAspProAlaProGlyValaGly	704
DB	2131	ATTCTGCTGTGTGCTTGGGGTGTCTTTGGGATCTCTCATCAAGCGACGGCAGCAG	2190	DB	3211	GAGGAGTATCTGTATCCCCCAGCAGGGCTTCTTCTGTCCAGACCTTGTCCCGGCGCTGG	3270
QY	705	GlyMetValHisHisArgHisArg	712	QY			

Db 3271 GGCATGTCACACAGCAGCCGC 3294
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RESULT 12

US-09-811-115-1
; Sequence 1, Application US/09811115
; Patent No. 6632979
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENE.034A
; CURRENT APPLICATION NUMBER: US/09/811.115
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9274
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Vector Sequence
US-09-811-115-1

Alignment Scores:
Pred. No.: 0 Length: 9274
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 4 Gaps: 1

US-09-493-480-7 (1-712) x US-09-811-115-1 (1-9274)

Qy 1 MetGluLeuAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
Db 1731 ATGGAGCTGGCGGCTTGTGCGCTGGGGCTCTCTCTCGCCCTCTTGGCCCGGAGCC 1790
Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetIysLeuArgLeuProAlaSerProGlu 40
Db 1791 GCGAGCAGCCCAAGTGTGCACCGGACAGACATGAAGCTGGGGCTCCCTGCCAGTCCCGAG 1850
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrglnGlyCysGlnValValGlnGlyAsnLeu 60
Db 1851 ACCCACTGGACATGCTCCGCCACTCTTACAGGGCTGCCAGGTGGTGCGAGGGAACCTG 1910
Qy 61 GluLeuThrTyrrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
Db 1911 GAACCTACCTACCTGCCACCAATGTCAGCCCTGTCTCTCTGAGGATATCCAGGAGTG 1970
Qy 81 GlnGlyTyrrValLeuLeuAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 1971 CAGGGCTACGTGCTCATCGCTCACAAACCAAGTGGAGCGAGTCCCACTGCAGAGCTGGCG 2030
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrrAlaLeuAlaValLeuAspAsnGly 120
Db 2031 ATTGTGGAGGACCCAGCTCTTTTGGAGCAACATATGCCCTTGGCCGTGCTAGACAAATGGA 2090
Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 2091 GACCCGCTGAACATACACCCCTGTCCAGCGGCCCTCCCGCAGGAGGCTGGGGAGCTG 2150
Qy 141 GlnLeuArgSerLeuThrGluIleLeuIysGlyValLeuLeuGlnArgAsnProGln 160
Db 2151 CAGCTTCGAGCCCTCACAGAGATCTTCAAAAGAGAGGGGTCTTGTATCCAGCGGAACCCCGAG 2210
Qy 161 LeuCysTyrrGlnAspThrIleLeuTrpIysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 2211 CTCTGCTACCGGACAGATTTTGGAGAGGACATCTTCCAAAGAACCAACCACTGGCT 2270

Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 2271 CTCACACTGATAGACACCAACCGCTCTCGGGCTTCCACACCCCTGTGTCTCCGATGTGTAAG 2330
Qy 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 2331 GGCTCCCGCTCTCTGGGAGAGAGTTCTGAGGATTTCTAGAGCTGACGGCTGACCGCACTGTCTGT 2390
Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysHisGlnGlnCys 240
Db 2391 GCGGTGGCTGTGCCCGCTGCAAGGGCCACTGCCCACTGACTGTGCTCCATGAGCAGTGT 2450
Qy 241 AlaAlaGlyCysThrGlyProIysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 2451 GCTGCCGCTGCACGGCCCAAGCACTCTGACTGCTGCTGGCTGCTCCACTTCAACCAAC 2510
Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrrAsnThrAspThrPheGlu 280
Db 2511 AGTGCATCTGTGAGCTGACTGCCAGCCCTGGTACCTACCAACAGACAGCTTTGAG 2570
Qy 281 SerMetProAsnProGluGlyArgTyrrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 2571 TCCATGCCCAATCCCGAGGGCGGTATACATTTGGGGCCAGCTGTGTGACTGCTCTGCC 2630
Qy 301 TyrAsnTyrrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db 2631 TACAACCTACCTTTCTACGGAGCTGGGATCTGACACCTCTGCTGCCCTGCAACACCA 2690
Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluIysCysSerIysProCysAlaArg 340
Db 2691 GAGGTGACAGCAGAGGATGGAACAAGCGGTGTGAGAGTGAGAGGCTGAGAGGCTTGGCCCGA 2750
Qy 341 ValCysTyrrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
Db 2751 GTGTGCTATGCTCTGGGCTGAGGACCTTGGAGAGGTGAGGGGAGTACCAGTGCCTCAAT 2810
Qy 361 IleGlnGluPheAlaGlyCysIysIysIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 2811 ATCCAGGAGTTTGTCTGCTGCAAGAAGATCTTTGGGAGCTTGGCATTTCTGCCGAGAGC 2870
Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
Db 2871 TTTGATGGGAGCCAGCCTCCAACTGCCCGCTCCAGCCAGAGCAGCTCCAAAGTGT 2930
Qy 401 GluThrLeuGluGluIleThrGlyTyrrLeuTyrrIleSerAlaTrpProAspSerLeuPro 420
Db 2931 GAGACTCTGGAAGAGATCACAGTTTACCTATACATCTCAGCATGTCGCGACAGCTGCT 2990
Qy 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
Db 2991 GACCTCAGCGCTTTCCAGAACCTGCAAGTAATCCGGGGAGCAATTTCTGCACCAATGGCGCC 3050
Qy 441 TyrrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
Db 3051 TACTGCTGACCCCTGCAAGGGCTGGGCTACAGCTGGCTGGGGCTGGGCTCACTGAGGGA 3110
Qy 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
Db 3111 CTGGCAGTGACTGGCCCTCATCCACCAACACCCACCTCTGCTCTGTCACACAGGTG 3170
Qy 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
Db 3171 CCCTGGGACCAAGCTCTTTGGGAACCCGACCAAGCTCTGCTCCACATGCTCCCAACCGGCA 3230
Qy 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
Db 3231 GAGGACAGTGTGTGGGAGGGCTGGGCTGCTGCCACAGCTGTGCGCCCGGAGGCACTGC 3290
Qy 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Db 3291 TGGGGTCCAGGGCCCAACCACTGTCTCACTGACCGAGTCTCTTCCGGCCGAGGAGTGC 3350
Qy 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrrValAsnAlaArgHisCys 560

Db 3351 GTGAGGAAATCCCGAGTACTCAGGGGCTCCCGAGGAGTATGTGAATGCCAGGCACTGT 3410
QY 561 LeuProCysHisProGluCysGlnProGlnAnGlySerValThrCysPheGlyProGlu 580
Db 3411 TTGCGGTGCCACCTCTAGTGTGTCAGCCCGAGATGGCTCTGTCGTCTGTTGGACCGAG 3470
QY 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
Db 3471 GCTGACCACTGTGTGGCTGTGGCCCTATTAAGGACCTCTCTCTGCGTGGCCGCTGC 3530
QY 601 ProSerGlyValLysProAspLysSerTyrMetProLleThrLysPheProAspGluGlu 620
Db 3531 CCCAGCGTGTGAACCTCTGCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG 3590
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLysAspLys 640
Db 3591 GGCGCATGCCAGCTTGGCCCATCACTCACTGACCCACTCTGTGTGGACTGTGATGACAG 3650
QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
Db 3651 GGCTGCCCGCGAGCAGAGAGCCAGCCCTCTGACGTCCATCTCTGCGTGGTGGC 3710
QY 653 653 653
Db 3711 ATTCTGCTGCTGGTCTTGGGGGTGGTCTTTTGGGATCTTCATCAAGCGAGCGCAGCAG 3770
QY 653 653 653
Db 3771 AAGATCCGGAAGTACACGATGCGGAGACTGCTGTCAGGAAACGAGCTGTGTGGAGCGCGCTG 3830
QY 653 653 653
Db 3831 ACACCTAGCGGAGCATGCCCAACGAGCGCAGATGCGGATCTCTGAAGAGAGCGAGCTG 3890
QY 653 653 653
Db 3891 AGGAAGTGAAGGTCTTGATCTGGCGCTTTTGGCACAGTCTACAAGGCACTGTGATC 3950
QY 653 653 653
Db 3951 CCTGATGGGAGATGTGAATTCAGTGGCCATCAAGTGTTCAGGGAAACACATCC 4010
QY 653 653 653
Db 4011 CCCAAGCCCAAGAAATCTTAGACGAAGCATAGTGTGCTGTGTGGCTCCCCA 4070
QY 653 653 653
Db 4071 TATGTCTCCGCTTCTGGGCATCTGCTGACATCCAGGTGAGCTGTGTGACACAGCTT 4130
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Db 4131 ATGCCCTATGCTGCTCTTAGACCATGTCCGGAAACCGCGGAGCCCTGGGCTCCAG 4190
QY 653 653 653
Db 4191 GACCTGCTGAATGCTGTATGAGATTTGCAAGGGGATGAGCTACCTGAGGATGTGCGG 4250
QY 653 653 653
Db 4251 CTCTGACACAGGAGCTTGGCGCTGCGAACTGCTGTGTCAAGAGTCCCAACATGTCAA 4310
QY 653 653 653
Db 4311 ATTACAGACTTGGGCTGGCTGGCTGTGGACATTTGACGACAGAGTACCATGCAGAT 4370
QY 653 653 653
Db 4371 GGGGGCAAGGTGCCCATCAAGTGTGATGGCGCTGGAGTCCATTTCTCGCGCGGCTTACC 4430
QY 653 653 653

Db 4431 CACCAGAGTATGTGTGGAGTATGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 4490
QY 653 653 653
Db 4491 AAACCTTAGCATGGATCCAGCCCGGAGATCCCTGACCTCTCGAAAAGGGGAGCGG 4550
QY 653 653 653
Db 4551 CTGCCCCAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGTCAATGTTGGATG 4610
QY 653 653 653
Db 4611 ATTGACTCTGAATGTGGCCAGATTTCCGGGAGTTGGTGTCTGAATTTCTCCGCAATGGCC 4670
QY 654 654 654
Db 4671 AGGACCCCCAGCGCTTTGTGTCTCATCCAGATGAGGACTTGGGCCACGACGATCTT 4730
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 4731 GACGACCTTTCTACCCGCTCACTGCTGGAGGACGATGATGGGGACCTGGTGGATGCT 4790
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 4791 GAGGAGTATCTGTTACCCAGCAGCGGCTTCTCTCTCCAGACCTGCCCCGGCGCTGGG 4850
QY 705 GlyMetValHisHisArgHisArg 712
Db 4851 GGCATGGTCCACACAGCGCACCGC 4874
RESULT 13
US-09-146-283-3
; Sequence 3, Application US/09146283
; Patent No. 5976546
; GENERAL INFORMATION:
; APPLICANT: Laus, Reiner
; APPLICANT: Ruegg, Curtis L.
; APPLICANT: Wu, Hongyu
; TITLE OF INVENTION: Immunostimulatory Compositions
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dehlinger & Associates
; STREET: 350 Cambridge Ave. Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,283
; FILING DATE: 03-SEPT-1998
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Judge, Linda R.
; REGISTRATION NUMBER: 42,702
; REFERENCE/DOCKET NUMBER: 7636-0010.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2385 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:

ORGANISM: homo sapiens
 INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig. 8
 US-09-146-283-3

Alignment Scores:

Pred. No.: 0 Length: 2385
 Score: 3632.00 Matches: 659
 Percent Similarity: 98.65% Conservative: 0
 Best Local Similarity: 98.65% Mismatches: 5
 Query Match: 91.86% Indels: 4
 DB: 2 Gaps: 2

US-09-493-480-7 (1-712) x US-09-146-283-3 (1-2385)

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Qy 1 MetGluLeuAlaLeuCysArgTrpGlyLeuLeuAlaLeuLeuProGlyAla 20
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Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetIlySerLeuArgLeuProAlaSerProGlu 40
Db 71 GCGAGCACCCAGGTGTGCACGGGCACACATGAGAGCTGGGGCTCCCTGCCAGTCCCGAG 130

Qy 41 ThrHisLeuAspMetLeuArgHisLeuTrpGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 131 ACCACCTGGACATGCTCCGCCACTCTTACCAGGGCTGCGAGGTGGTGCAGGGAACTG 190

Qy 61 GluLeuThrTrpLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 191 GNACTCACTTACCTGCCCAATGCCAGCTGTCTCTCTGCGAGGATATCCAGGAGGTG 250

Qy 81 GlnGlyTrpValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 251 CAGGGCTACCTGCTCATCGCTCACACCAAGTACGAGGAGGTCCCACTGCAGAGCTCGG 310

Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTrpAlaLeuAlaValLeuAsnGly 120
Db 311 ATTGTGGAGGCCACCGAGCTCTTTGAGGACAACTATATGCCCTGGCGGTGAGACATGGA 370

Qy 121 AspProLeuAsnAnthrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 371 GACCCGCTGAACAATACCAACCCCTGTACAGGGGCTCTCCAGGAGGCTCGGGAGCTG 430

Qy 141 GlnLeuArgSerLeuThrGluIleLeuIlyGlyGlyValLeuIleGlnArgAsnProGln 160
Db 431 CAGCTTCGAAGCCTCACAGAGATCTTGAAGAGAGGGGTCTTGATCCAGGGAAACCCAC 490

Qy 161 LeuCysTrpGlnAspThrIleLeuTrpIlyAsnIlePheHisIlyAsnGlnLeuAla 180
Db 491 CTCTGCTACAGGACACGATTTTGTGAAGACATCTTCACAGAAACACCACTGGCT 550

Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 551 CTCACACTGATAGACACCAACCGCTCTCGGGCTCGCCACCCCTGTCTCCGATGTGTAG 610

Qy 201 GlySerArgCysTrpGlyGlySerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 611 GGCTCCCGCTGCTGGGAGAGAGTCTCAGAGATTGTTCAGAGCCTGACGCGCACTGTCTGT 670

Qy 221 AlaGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
Db 671 GCGGTGGCTGTGCGCCCTGCAAGGGGCCACTGCGCCACTCACTGCTGCCATGAGCAGTGT 730

Qy 241 AlaAlaGlyCysThrGlyProIlyHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 731 GCTCGGGCTGCAAGGGCCCCAGCACTCTGACTGCTCGCTGGCTCGCTCCACTTCAACAC 790

Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 791 AGTGGCATCTGTGAGCTGCACTGCCCAAGCTGCTGCTCACTCACTACCAACACAGACAG 850

Qy 281 SerMetProAsnProGluGlyArgTrpThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 851 TCCATGCCCAATCCCGAGGGCCGGTATACATTCGGGCGCCAGCTGTGTGACTGCGCTGTGCC
  
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Qy 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
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Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGlnCysCysSerIlyProCysAlaArg 340
Db 971 GAGGTGACAGCAGAGGATGGAAACACAGCGGTGTGAGAGTGCAGCAAGCCCTGTGTCCCGA 1030

Qy 341 ValCysTrpGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
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Qy 361 IleGlnGluPheAlaGlyCysIlyIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 1091 ATCCAGGAGTTTGTGTGCTGCACAGAGATCTTTGGAGCCTGGCATTTCTGCGGAGAGC 1150

Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
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Qy 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
Db 1271 GACTCTAGGCTCTCCAGAACCTGCAAGTAATCCGGGACGAATCTTCACCAATGGCGCC 1330

Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
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Qy 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
Db 1391 CTGGGAGTGGACTGGGCTCATCCACATTAACCCACCTCTGCTTGTGTGCACAGGTG 1450

Qy 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
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Qy 541 ValGluCysArgValLeuGlnGlyLeuProArgGluTrpValAsnAlaArgHisCys 560
Db 1631 GTGGAGGAATGCCAGTACTGACGGGCTCCCGAGGAGTATGTGAATGCCAGGCACTGT 1690

Qy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
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Qy 581 AlaAspGlnCysValAlaCysAlaHisTrpIlyAspProProPheCysValAlaArgCys 600
Db 1751 GCTGACCCAGTGTGGGCTGTGCCCACTATAAGACCCCTCCCTTCTGGTGGCCGCTGC 1810

Qy 601 ProSerGlyValIlyProAspLeuSerTyrMetProIleTrpIlyPheProAspGluGlu 620
Db 1811 CCCAGCGGTGGAACCTGACCTCTCTACATGATGCCATCTGGAATTTCCAGATGAGGAG 1870

Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
Db 1871 GGGCATGCGCAGCTTGGCCCCCACTCACTGCACCCACTCTCTGTGTGGACTGTGATGACAAG 1930

Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSerGlnAsnGluAspLeuGlyPro 660
Db 1931 GGCTGCCCCCGGAGGAGGAGCGCCCTCTGACGCTCCCTCGAG-----GCACCC 1981
  
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Db 1271 GACCTCAGCGCTCTTCAGAACCTTCAGAGTAATTCGGGACGAATTCGCAATGGCGCC 1330
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Db 1331 TACTCGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGCTCACTCAGGGAA 1390
Qy LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
Db 1391 CTGGGAGTGGACTGGCCCTCATCCACCAATACACCCACTCTGCTTGGGCGCACGGTG 1450
Qy ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
Db 1451 CCTGGGACCGAGCTCTTCGGAAACCGCACCAAGCTCTGCTCCACTGCAACCGGCCA 1510
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Db 1511 GAGGACGAGTGTGTGGCGAGGGCTGGCCCTGCCACCACTGTGTGGCGGCGGCACTGC 1570
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Db 1691 TTGGCGTGCACCTGAGTGTGAGCCCAATGGCTCAGTACCTGTTTGGACCGAG 1750
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Db 1811 CCAGCGGTGTGAACCTGACCTCTCTACATGCCCACTTGGAGTTTCCAGATGAGGAG 1870
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RESULT 15

US-09-344-195-3

; Sequence 3, Application US/09344195

; Patent No. 6210662

; GENERAL INFORMATION:

; APPLICANT: Laus, Reiner

; Wu, Hongyu

; Rugg, Curtis L.

; TITLE OF INVENTION: Immunostimulatory Compositions

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dehlinger & Associates

; STREET: 350 Cambridge Ave. Suite 250

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/344,195
; FILING DATE: 24-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,283
; FILING DATE: 03-SEPT-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Judge, Linda R.
; REGISTRATION NUMBER: 42,702
; REFERENCE/DOCKET NUMBER: 7636-0010.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2385 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; INDIVIDUAL ISOLATE: GM-CSP-HER-2 fusion gene; Fig. 8
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-344-195-3

Alignment Scores:

Pred. No.:	0	Length:	2385
Score:	3632.00	Matches:	659
Percent Similarity:	98.65%	Conservative:	0
Best Local Similarity:	98.65%	Mismatches:	5
Query Match:	91.86%	Indels:	4
DB:	3	Gaps:	2

US-09-493-480-7 (1-712) x US-09-344-195-3 (1-2385)

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Qy	41	ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu	60
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Qy	61	GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal	80
Db	191	GAACCTACCTTACCTGCCCAATGCCAGCTGTCTCTCTGCCAGGATATCCAGAGGTG	250
Qy	81	GlnGlyTyrValLeuLeuAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100
Db	251	CAGGGCTAGCTGTCTATGCTCAACCAAGTAGGCGAGTCCACCTGCAGAGGCTCGG	310
Qy	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120
Db	311	ATTGTGGAGGACCCAGCTTTTGGAGACACTATGCTTGGCCCTGGCCGTGTAGACATGGA	370
Qy	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140
Db	371	GACCCCTGAAACAATACCACTCCCTGTACAGGGGCTCCCGCAGGAGGCTCGCGAGCTG	430
Qy	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuLeuGlnArgAsnProGln	160
Db	431	CAGCTTCGAAGCCTCAGAGATCTTGAAGAGGAGGGGTCTTGATCCAGCGGAAACCCAG	490
Qy	161	LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnAsnGlnLeuAla	180

Db 491 CTCTGCTACACAGACACGATTTTGTGGAGGACATCTTCCACAGAACACACCGCTGGCT 550
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Db 551 CTCACACTGATAGACACACCGCTCTCGGGCTGGCCACCCCTGTTCTCCGATGTGAAG 610
Qy 201 GlySerArgCysTrpGlyGlySerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 611 GGCTCCCGCTCTGGGGAGAGAGTTCTCAGGANTTGTACAGAGCTGACCGCAGCTGTCTGT 670
Qy 221 AlaGlyGlyCysAlaAArgCysGlyProLeuProThrAspCysCysHisGluGlnCys 240
Db 671 GCCGTGCTGTGCCCGCTGCAAGGGGCCACTGCCACTGTGCTGCTGCTGCTGCTGCTGCT 730
Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 731 GCTGCCGCTGCACGGGCCCCAAGCACCTCTGACTGCTGGCTGGCTGCTGCCACTTCAACCCAC 790
Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 791 AGTGGCATCTGTGAGCTGCACCTGCCAGCCCTGGTCACTTACCAACACACAGACACGTTTGAG 850
Qy 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 851 TCCATGCCCAATCCCGAGGGCCGGTATACATTCGGCGCCAGCTGTGTGACTGCCCTGTCCC 910
Qy 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db 911 TACAACCTACCTTTCTACGGAGCTGGGATCCTGCACCCCTGCTGCTGCCCTGCACACCAA 970
Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
Db 971 GAGGTGACACAGAGATGGAACACAGCGGTGTGAGAGTGCAGCAAGCCCTGTGCCCGA 1030
Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
Db 1031 GTGTCTATGTGTGGGATGAGGACATTCGAGAGGTGAGGGCAGTTACCAAGTCCCAAT 1090
Qy 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
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Search completed: June 7, 2004, 15:45:45
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 7, 2004, 13:54:19 ; Search time 643.463 Seconds
(without alignments)
5047.907 Million cell updates/sec

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Delop 6.0 , Delext 7.0

Searched: 2995936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters: 5991872

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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US-10-207-498-5
; Sequence 5, Application US/10207498
; Publication No. US20030143568A1
; GENERAL INFORMATION:
; APPLICANT: Elizabeth Singer
; APPLICANT: Ralf Landgraf
; APPLICANT: Dennis J. Slamon
; APPLICANT: David Eisenberg
; TITLE OF INVENTION: METHODS AND MATERIALS FOR CHARACTERIZING
; FILE REFERENCE: 30448.103-US-UI
; CURRENT APPLICATION NUMBER: US/10/207,498
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/308,431
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3765
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

ALIGNMENTS

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5	3776	95.5	3768	9	US-09-930-125-1	Sequence 1, Appli
6	3776	95.5	3768	13	US-09-984-092-3	Sequence 3, Appli
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; Patent NO. US20020035736A1
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT.034A
; CURRENT APPLICATION NUMBER: US/09/811,115
; CURRENT FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-115-2

Alignment Scores:

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Score:	3776.00	Matches:	712
Percent Similarity:	67.94%	Conservative:	0
Best Local Similarity:	67.94%	Mismatches:	0
Query Match:	95.50%	Indels:	336
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US-09-493-480-7 (1-712) x US-09-811-115-2 (1-3768)

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Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
Db 1141 TTTGATGGGAGCCAGGCTCCAAACATGCTGCCCGCTCCAGCCAGAGCAGCTCCAGTGT 1200

Qy 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrrProAspSerLeuPro 420
Db 1201 GAGACTCTGGAAGAGATCACAGGTTCCTATATACATCTCAGCATGCGCCGACAGCTGCCT 1260
Qy 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
Db 1261 GACCTTCAGCGTCCTTCAGAACCTCGAGTAATCCGGGACGAAATCTGCACAAATGGCGCC 1320
Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
Db 1321 TACTCGCTGACCTGCAAGAGCTGGGCATCAGCTGGCTGGGCTGCCTCACTGAGGGAA 1380
Qy 461 LeuGlySerGlyLeuAlaLeuIleHisIleHisThrHisLeuCysPheValHisThrVal 480
Db 1381 CTGGGACGTGGAGCTGCCTCATCCACCAATACACCCACCTCTGCTTCGTGCACAGGTG 1440
Qy 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
Db 1441 CCCTGGGACCAAGCTCTTTCCGAACCCGACCAAGCTCTGCTCCACACTGCCACCGGCA 1500
Qy 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
Db 1501 GAGGACGAGTGTGGGCGAGGGCTGGCTGCCACCAAGCTGTGGCTGGGAGGCACTGC 1560
Qy 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Db 1561 TGGGCTCCAGGCGCCCACTGCTCACTGACCACTGCTTCCTGGGCGCCAGGAGTGC 1620
Qy 541 ValGluGluCysAspValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
Db 1621 GTGGAGGAATGCCGAGTACTGCGAGGGCTCCCGAGGAGTATGTGAAATGCCAGGCACTGT 1680
Qy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 1681 TTGCGTGCCACCTCTGAGTGTGAGCCCGAGGATGCTCAGTGACCTGTTTGGACCGGAG 1740
Qy 581 AlaAspGlnCysValAlaCysAlaHisTyrIleAspProProPheCysValAlaArgCys 600
Db 1741 GCTGACCACTGTGTGGCTGTGCCCACTATAGGACCTCTCCCTCTGCTGGCGCCGCTGC 1800
Qy 601 ProSerGlyValIleProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
Db 1801 CCCAGGCTGTGAAACCTGACCTCTCTACATGCCCACTGAGAGTTCCAGATGGAG 1860
Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspPheLys 640
Db 1861 GGCGCATGCCAGCTTTGCCCACTGACCCACTGCTGTGTGGAACCTGGATGACAAG 1920
Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
Db 1921 GGCTGCCCGCGGAGCAGAGAGCCAGCCCTCTGACGTCCATCTCTCTGCGGTGTGGC 1980
Qy 653 653 653
Db 1981 ATTCTGTGTCGTGGTCTTTGGGGGTGGTCTTTGGGATCTCTATCAGCGACGGCAGCG 2040
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Qy 653 653 653
Db 2101 ACACCTAGCGGAGCGATGCCCAACGAGGCGCAGATCGGATCCTTGAAAGAGACGGAGCTG 2160
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Qy 653 653 653
Db 2461 GACCTGCTGAATGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGAGGATGTGGG 2520
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Db 2521 CTCGTACACAGGACTTGGCGCTCGGAACTGTCTGTCTCAAGAGTCCCAACCATGTCAAA 2580
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Db 2641 GGGGCAAGGTGCCCATCAAGTGGATGGGCTGGAGTCCATTCTCGCGCGGGTTTACC 2700
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Db 2941 AGGACCCCCAGCGCTTTGTGGTCAATCCAGAAATGAGGACTTGGGCCAGCCAGTCCCTTG 3000
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Db 3001 GACAGCACTTCTACCGCTCACTGCTGGAGACGATGACATGGGAGACCTGGTGGATGCT 3060
Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGTAACCCAGCAGGGCTTTCTTCTGTCAGACCTTGCCTGGCGCTGGG 3120
Qy 705 GlyMetValHisHisArgHisArg 712
Db 3121 GGCATGGTCCACACAGGACCGC 3144

RESULT 4

US-09-854-356-9
Sequence 9, Application US/09854356
Patent No. US20020177567A1
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Dirk
APPLICANT: Corixa Corporation
APPLICANT: SmithKline Beecham Biologicals S. A.
TITLE OF INVENTION: HER-2/neu Fusion Proteins
FILE REFERENCE: 014058-009610PC
CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT FILING DATE: 2001-05-09

; PRIOR APPLICATION NUMBER: US 09/493,480
 ; PRIOR FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: US 60/117,976
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 9
 ; LENGTH: 3768
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(3768)
 ; OTHER INFORMATION: human HER-2/neu protein
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(1959)
 ; OTHER INFORMATION: extracellular domain (ECD) of human HER-2/neu
 ; NAME/KEY: misc feature
 ; LOCATION: (2026)..(3765)
 ; OTHER INFORMATION: intracellular domain (ICD) of human HER-2/neu
 ; NAME/KEY: misc feature
 ; LOCATION: (2968)..(3144)
 ; OTHER INFORMATION: phosphorylation domain (PD) of human HER-2/neu
 ; NAME/KEY: misc feature
 ; LOCATION: (2968)..(3144)
 ; OTHER INFORMATION: preferred portion of the phosphorylation domain
 ; OTHER INFORMATION: (delta PD) of human HER-2/neu
 ; US-09-854-356-9

Alignment Scores:
 Pred. No.: 0 Length: 3768
 Score: 3776.00 Matches: 712
 Percent Similarity: 67.94% Conservative: 0
 Best Local Similarity: 67.94% Mismatches: 0
 Query Match: 95.50% Indels: 336
 DB: 9 Gaps: 1

US-09-493-480-7 (1-712) x US-09-854-356-9 (1-3768)

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DB	1	ATGGAGCTGGCGGCTTGTGCGCGCTGGGGCTCTCTCTCGCCCTCTTGGCCCCCGAGCC	60
QY	21	AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu	40
DB	61	GGGAGCAACCACTGTGCACCGGCACAGACATGAGCTGGGGCTCCCTGCGCATCCCGAG	120
QY	41	ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu	60
DB	121	ACCCACCTGCACATGCTCCGCCACCTCTACCAAGCTGGCGGCTGGCGGTCAGAGGAACTG	180
QY	61	GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal	80
DB	181	GAACCTACCTTACCTGGCCCAACATATGCAGCTGTGTCTTCCTGAGGATATCCAGGAGTG	240
QY	81	GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100
DB	241	CAGGGCTACGTGCTCATGGCTCACACCAAGTGGCGAGGTCCCACTGCAGAGGCTGGCG	300
QY	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120
DB	301	ATTGTGCGAGGCCACCCAGCTCTTTGAGGACAACTATATGCTGGCGGCTGGCGGTCAGTGA	360
QY	121	AspProLeuAsnThrThrProValThrGlyValaSerProGlyLeuArgGluLeu	140
DB	361	GACCCCTGAACAATACCACTGTCACAGGGGCTTCCCGAGAGGCTTGGCGGAGCTG	420
QY	141	GlnLeuArgSerLeuThrGluLeuLeuLysGlyValLeuIleGlnArgAsnProGln	160
DB	421	CAGCTTCGAAGCTTCACAGAGATCTTGAAAGAGGGGTCTTGATCCAGCGGAACTCCAG	480
QY	161	LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnGlnLeuAla	180

DB	481	CTCTGTACCAGGACACGATTTTGTGGAAGACATCTTCCACAAGAAACAACAGCTGGCT	540
QY	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
DB	541	CTCAGCTGATAGACACCAACCGCTCTGGGGCTGCCACCCCTGTTCTCCGATGTGAAG	600
QY	201	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220
DB	601	GGCTCCGCTGCTGGGAGAGAGTTCTGAGGATTTGTCAGAGCCTGACGCGCACTGCTGT	660
QY	221	AlaGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	240
DB	661	GCCGGTGGCTGTGCCCTGCAAGGGGCCACTGCCCCTGACTGCTGTCATGAGCAGTGT	720
QY	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
DB	721	GCTGCCGGCTGCACGGGCCCAAGCACTCTGACTGCTGGCTGCTCCCTTCAACCCAC	780
QY	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280
DB	781	AGTGGCATCTGTGAGCTGCACCTGCCAGCCCTGGTCACTTACAAACACAGACACGTTTGA	840
QY	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300
DB	841	TCCATGCCCAATCCGAGGGCCGGTATACATTCGGCGCCAGCTGTGTGACTGCTGTCCC	900
QY	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
DB	901	TACAACTACCTTCTACGGAGCTGGGATCTGCACCCCTGCTGCCCCCTGCACAAACCA	960
QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340
DB	961	GAGTGACAGCAGAGGATGAAACACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGTGCCG	1020
QY	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
DB	1021	GTGTGCTATGCTTGGGCATGAGGACCTTCGAGAGGTGAGGGGAGTTTACAGTGCCCAAT	1080
QY	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380
DB	1081	ATCAGAGGTTTGTGCTGCAAGAGATCTTTGGGAGCTGGCATTTCTGCCGAGAGC	1140
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400
DB	1141	TTTGTATGGGACACCGCTCCAAACACTCCCGCTCCAGCCAGAGCAGCTCCAAGTGT	1200
QY	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro	420
DB	1201	GAGACTCTGGAAGAGATCACAGGTATACCTATACATCTCAGCATGGCCGAGCAGCTGCCT	1260
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440
DB	1261	GACCTCAGCTCTTCCAGAACCTGCAAGTAACTCCGGGAGCGAATTTCTGCACATGGGCGC	1320
QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
DB	1321	TACTCGCTGACCTTCGAAGGGCTGGGCATCAGCTGGCTGGGGCTGCGCTCTCATGAGGAA	1380
QY	461	LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal	480
DB	1381	CTGGGAGTGGATGGGCTTCATCCACCAACCCACCTCTGCTTCTGTCACACCGTG	1440
QY	481	ProTyrAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
DB	1441	CCCTGGGACCGAGCTCTTTCGNAACCCGACCAAGCTCTGCTCCACACTGCGCAACCGGCA	1500
QY	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
DB	1501	GAGGACGAGTGTGGCGGAGGGCTGGCTGGCCACCGCTGCTGGCGGCCGAGGACCTGC	1560
QY	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
DB	1561	TGGGGTCCAGGGGCCCACTGAGTGTGCACTGACAGCGAGTTCTTCTTCGGGGCCAGGAGTC	1620


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Qy 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
Db 1621 GTGAGGAATGCGAGTACTGCGGGCTCCAGGGAGTATGTGAATGCCAGGCACCTGT 1680
Qy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 1681 TTGGCGTCCACCCCTGAGTGTGAGCCCGCAGATGGCTCAGTGACCTGTTTGGACCGGAG 1740
Qy 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
Db 1741 GCTGACCAAGTGTGGCCCTGTGCCACCTATAGGACCTCCCTTCTGGTGGCCGCTGC 1800
Qy 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
Db 1801 CCCAGCGGTGGAACCTGACCTCTCTACATGATGCCCATCTGGAAGTTTCCAGATGAGGAG 1860
Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
Db 1861 GGCGCATGCCAGCCTTGCCCCATCACTGACCCCACTCTGTGTGGACCTGGATGACAAG 1920
Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
Db 1921 GGCTCCCGCCGACGAGAGAGCCAGCCCTCTGACGTCATCTCTCGGTGGTGGC 1980
Qy 653 ----- 653
Db 1981 ATTCGTGCTGCTGTGCTGTGGGGTGTCTTTTGGATCTCTCATCAAGCGCGCAGCAG 2040
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Db 2041 AAGATCCGGAAGTACACGATCGGAGACTGCTGCAGGAACCGAGCTGGTGGAGCGGTG 2100
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Db 2101 ACACCTAGCGGAGCGATGCCCAACCGGCGCAGATCGGATCCTGAAAGAGACGGAGCTG 2160
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Db 2281 CCCAAGCCCAACAAGAAATCTTAGACGAGCATAGTGTGCTGGTGGCTCCCCA 2340
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Db 2401 ATGCCCTATGGTGCCTCTTAGACCATGTCCGGGAAAAACGGGAGCGCTGGGCTCCAG 2460
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Db 2521 CTGCTACACAGGACCTTGGCGCTCGGAAGCTGCTGTGTCAAGAGTCCCAACCATGTCAAA 2580
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Db 2881 ATTGACTCTGAATGTGGGCCAAGATTCCGGAGTGGTGTCTGAAATCTCCCGCATGGCC 2940
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Db 2941 AGGAGCCCCCAGCGCTTTGTGTGTATCCAGATGAGGACTTGGGCCCGCAGCATGCTCTTG 3000
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Db 3001 GACAGCACCTTCTACCGCTCACTGTGGAGGACGATGACATGGGGGACCTGTGTGATGCT 3060
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RESULT 5
US-09-930-125-1
; Sequence 1, Application US/09930125
; Publication No. US20020193329A1
; GENERAL INFORMATION:
; APPLICANT: Hand-Zimmerman, Susan
; APPLICANT: Cheever, Martin A.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Vedwick, Thomas S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS
; OF HER-2/NEU-ASSOCIATED MALIGNANCIES
; FILE REFERENCE: 210121.544
; CURRENT APPLICATION NUMBER: US/09/930,125
; CURRENT FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-09-930-125-1
Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 1 Gaps: 1
US-09-493-480-7 (1-712) x US-09-930-125-1 (1-3768)
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Db 1 ATGGAGCTGGCGCTTGTGGCGCTGCGGCTCTCTCTCGCCCTCTTGTGCCCCCGGAGCC 60
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Qy	21	AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu	40
Db	61	GGGAGCACCCAAAGTGTGCACGGCACAGACATGAAGCTGGCGTCCCTGCGAGTCCCGAG	120
Qy	41	ThrHisLeuAspMetLeuArgHisLeuTyrglnGlyCysGlnValValGlnGlnGlyAsnLeu	60
Db	121	ACCACCTGGACATGCTCCGGCCACTCTAC CAGGGCTGCCAGGTGGTG CAGGGAAACCTG	180
Qy	61	GluLeuThrTyrrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal	80
Db	181	GAATCTACCTACCTGCCCAACCAATGCCAGCTGTCTCTCTGCAGGATATCCAGGAGGTG	240
Qy	81	GlnGlyTyrrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100
Db	241	CAGGGCTACGTGCTCATCGCTCA CAACCAAGTGAGGCAGGTCCCACTGCAGAGGCTCGG	300
Qy	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrrAlaLeuAlaValLeuAspAsnGly	120
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Qy	121	AspProLeuAsnAsnThrThrProValThrGlyValaSerProGlyGlyLeuArgGluLeu	140
Db	361	GACCCGCTGAACAATACACCCCTGTGCAGGGGCTCCCCAGGAGGCTGCGGGAGCTG	420
Qy	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln	160
Db	421	CAGCTTCGAGGCTTCACAGAGATCTTGAAAGGAGGGGTCTTGATCCAGCGGAACCCCGAG	480
Qy	161	LeuCysTyrrGlnAspThrIleLeuTrpIysAspIlePheHisLysAsnAsnGlnLeuAla	180
Db	481	CTCTGCTACCAGGACACAGATTTGTGGAAGGACATCTTCCACAAGAACAACCACTGGCT	540
Qy	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
Db	541	CTCACACTGATAGACACAACACCGCTCTCGGGGCTGCCACCCCTGTCTCGAGATGTGAAG	600
Qy	201	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220
Db	601	GGCTCCCGCTCTGGGAGAGAGTTCAGAGGATGTG CAGGCTGCAGCGGCACCTGCTGT	660
Qy	221	AlaGlyGlyCysAlaAryCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	240
Db	661	GCCGCTGGCTGTGCGCGCTGCAAGGGCCACTGCGCCACTGACTGCTGCCATAGACAGTGT	720
Qy	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
Db	721	GCTGCCCGGCTGCACGGGGCCCAAGCACTCTGACTGCTCGCTGGCTGCCCTCCACTTCAC	780
Qy	261	SerGlyIleCysGluLeuLeuHisCysProAlaLeuValThrTyrrAsnThrAspThrPheGlu	280
Db	781	AGTGGCATCTGTGAGCTGCATGCCCCAGCCCTGTGTCACTTACAACA CAGACACGTTTGAG	840
Qy	281	SerMetProAsnProGluGlyArgTyrrThrPheGlyAlaSerCysValThrAlaCysPro	300
Db	841	TCCATGCCCAATCCGAGGGCCGTATACATTTGGGGCCAGCTGTGTGACTGCTGTGCC	900
Qy	301	TyrrAsnTyrrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
Db	901	TACAACCTACCTTTCTACGGGACGTGGGATCCCTGCACCCCTCGTCTGCCCTCTGCACAA	960
Qy	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340
Db	961	GAGGTGACGCGAGGATGGAAACACGCGGTGTGAGAGTGTGCACAAGGCCCTGTGCCCGGA	1020
Qy	341	ValCysTyrrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
Db	1021	GTGTGCTATGCTCTGGGCATGGAGCACTTGGCAGAGGTGAGGGCAGTTTACCAGTGCCAAT	1080
Qy	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380
Db	1081	ATCCAGGAGTTTGTGGCTGCAAGAAATCTTTTGGGAGCCTGGCGATTTCTGCGGAGAGC	1140

QY	381	Phe	Asp	Gly	Asp	Pro	Ala	Ser	Asn	Thr	Ala	Pro	Leu	Gln	Pro	Glu	Gln	Leu	Gln	Val	Phe	400
DB	1141	T	T	T	G	A	T	G	G	G	A	C	C	A	C	A	C	T	G	C	C	1200
QY	401	Glu	Thr	Leu	Glu	Glu	Ile	Thr	Gly	Tyr	Leu	Tyr	Ile	Ser	Ala	Trp	Pro	Asp	Ser	Leu	Pro	420
DB	1201	G	A	G	A	C	T	T	G	A	G	A	T	C	A	C	A	T	C	T	C	1260
QY	421	Asp	Leu	Ser	Val	Phe	Gln	Asn	Leu	Gln	Val	Ile	Arg	Gly	Arg	Ile	Leu	His	Asn	Gly	Vala	440
DB	1261	G	A	C	T	C	A	G	A	C	T	G	C	A	A	T	C	C	G	G	A	1320
QY	441	Tyr	Ser	Leu	Thr	Leu	Gln	Gly	Leu	Gly	Y	Ile	Ser	Trp	Leu	Gly	Leu	Arg	Ser	Leu	Arg	460
DB	1321	T	A	C	T	C	G	T	C	A	C	C	C	T	G	C	A	T	C	A	G	1380
QY	461	Leu	Cys	Ser	Gly	Leu	Ala	Leu	Ile	His	Asn	Thr	His	Leu	Cys	Val	His	Thr	Val		480	
DB	1381	C	T	G	G	C	A	G	T	G	G	C	C	T	C	A	T	C	T	G	C	1440
QY	481	Pro	Trp	Asp	Gln	Leu	Phe	Arg	Asn	Pro	His	Gln	Ala	Leu	Leu	His	Thr	Ala	Asn	Arg	Pro	500
DB	1441	C	C	T	G	G	A	C	A	G	T	C	T	G	C	A	C	A	C	T	G	1500
QY	501	Glu	Asp	Glu	Cys	Val	Gly	Glu	Gly	Leu	Ala	Cys	His	Gln	Leu	Cys	Ala	Arg	Gly	His	Cys	520
DB	1501	G	A	G	A	C	A	G	T	G	T	G	G	C	C	T	G	C	C	A	G	1560
QY	521	Trp	Gly	Pro	Gly	Pro	Thr	Gln	Cys	Val	Asn	Cys	Ser	Gln	Phe	Leu	Arg	Gly	Gln	Glu	Cys	540
DB	1561	T	G	G	G	T	C	C	A	C	C	A	G	T	G	T	C	C	T	T	C	1620
QY	541	Val	Glu	Glu	Cys	Arg	Val	Leu	Gln	Gly	Leu	Pro	Arg	Glu	Tyr	Val	Asn	Ala	Arg	His	Cys	560
DB	1621	G	T	G	A	G	A	G	A	T	C	C	C	A	G	G	A	T	T	G	A	1680
QY	561	Leu	Pro	Cys	His	Pro	Glu	Cys	Gln	Pro	Gln	Asn	Gly	Ser	Val	Thr	Cys	Phe	Gly	Pro	Glu	580
DB	1681	T	T	G	C	G	T	G	C	A	C	C	A	T	G	G	T	C	A	G	C	1740
QY	581	Ala	Asp	Gln	Cys	Val	Ala	Cys	Ala	His	Tyr	Leu	Asp	Pro	Pro	Phe	Cys	Val	Ala	Arg	Cys	600
DB	1741	G	C	T	S	A	C	A	G	T	G	T	G	G	C	A	T	A	P	A	G	1800
QY	601	Pro	Ser	Gly	Val	Lys	Pro	Asp	Leu	Ser	Tyr	Met	Pro	Ile	Trp	Lys	Phe	Pro	Asp	Glu	Glu	620
DB	1801	C	C	C	A	G	C	G	T	G	A	A	C	T	C	T	C	A	T	G	A	1860
QY	621	Gly	Ala	Cys	Gln	Pro	Cys	Pro	Ile	Asn	Cys	Thr	His	Ser	Cys	Val	Asp	Leu	Asp	Asp	Lys	640
DB	1861	G	G	G	C	A	T	G	C	C	C	A	T	C	A	C	T	C	T	G	T	1920
QY	641	Gly	Cys	Pro	Ala	Glu	Gln	Arg	Ala	Ser	Pro	Leu	Thr	Ser							653	
DB	1921	G	G	T	G	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	1980
QY	653																				653	
DB	1981	A	T	T	C	T	G	T	G	T	C	T	T	T	G	G	A	T	C	T	A	2040
QY	653																				653	
DB	2041	A	A	G	A	T	C	G	G	A	G	T	A	C	G	A	T	G	C	T	G	2100
QY	653																				653	
DB	2101	A	C	A	C	T	A	G	C	G	A	G	C	A	T	G	C	G	A	T	C	2160
QY	653																				653	
DB	2161	A	G	S	A	G	T	G	A	A	G	T	G	T	G	A	T	C	T	T	G	2220
QY	653																				653	

QY 261 SerGlyLeuCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
DB 781 AGTGGCATCTGTAGCTGCACTGCCAGCCCTGGTCACTACCAACAGACAGACGTTTGG 840
QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
DB 841 TCCATGCCCATNTCCGAGGCGCGGTATACATTCCGGCGCCAGCTGTGTGACTGCTGTCCC 900
QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
DB 901 TACAACTACCTTTCTACGACAGTGGGATCTCGACCCCTCGTCTGCCCTCGCAACCA 960
QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
DB 961 GAGGTGACAGCAGAGGATGAACACACAGCGGTGTGAGAAAGTGCAGAGCCCTGTGCCCCGA 1020
QY 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
DB 1021 GTGTGCTATGTCTGGGCATGGAGCACTTCCGAGAGTGGAGCGATTACAGTGCAT 1080
QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
DB 1081 ATCCAGAGTTTGTGCTGCAAGAGATCTTTGGGAGCCCTGGCAATTTCTGCCGAGAGC 1140
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe 400
DB 1141 TTTGATGGGAGACCCAGCCCTCCACACTGCCGCCCTCCAGCCAGAGCAGCTCCAAAGTGT 1200
QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420
DB 1201 GAGACTCTGGAGAGATCACAGTTTACCTATATCATCTCAGCATGGCCGAGACGCTGCT 1260
QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
DB 1261 GACCTCAGCGCTCTTCCAGAACCTGCAAGTAATCCGGGAGCAATTTGCACAAATGGGCC 1320
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuGlyLeuArgSerLeuArgGlu 460
DB 1321 TACTCTGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGCTCCTCCTCAGG 1380
QY 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
DB 1381 CTGGGAGTGGACTGGCCCTCATCCACCATTAACCCACCTCTGCTTGTGTGCACAGGTG 1440
QY 481 ProTyrAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
DB 1441 CCCTGGGACCAGCTCTTTGGGAACCCGACCAAGCTCTGCTCCACACTGCGCAACCGGCCA 1500
QY 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
DB 1501 GAGGACAGTGTGTGGGCGAGGGCCCTGGCCCTGCCACCCAGCTGTGCCGCCGAGGGCACTGC 1560
QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
DB 1561 TGGGGTCCAGGGCCCAACCCAGTGTGTCACTGACCCAGTTCCTTCCGGGCCAGGAGTGC 1620
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
DB 1621 GTGGAGGATGCCAGTACTGCAAGGGCTCCCGAGGGAGTATGTGAATGCCAGGCACTGT 1680
QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
DB 1681 TTGCCGTGCCACCCTGAGTGTGACGCCCCAGAAATGGCTCAGTGACCTGTGTTTGGACGGG 1740
QY 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
DB 1741 GCTGACAGTGTGGCTGTGCCCATATPAGGACCTCCCTCTGCTGGGCCCGCTGC 1800
QY 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu 620
DB 1801 CCCAGCGGTGAAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG 1860
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640

DB 1861 GGCGCATGCCAGCTTGGCCCATCACTGACCCACCTCTCTGTGTGGACTGTGATGACAG 1920
QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
DB 1921 GGCTGCCCCCGCAGCAGAGAGCCAGCCCTCTGACGCTCCATCGTCTCTGCGGTGTGTC 1980
QY 653 ----- 653
DB 1981 ATTTCTGCTGCTGCTGCTTTGGGGTGGTCTTTTGGGATCTCTCATCAAGCAGCGGAGCAG 2040
QY 653 ----- 653
DB 2041 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACCGAGCTGCTGGAGCCGCTG 2100
QY 653 ----- 653
DB 2101 ACACCTAGCGGCGATGCCAACCCAGCGCGAGATGCGGATCTCTGAAAGAGACGAGCTG 2160
QY 653 ----- 653
DB 2161 AGGAAGGTGAAGTGTCTTGGATCTTGGGCTTTTGGCAGAGTCTCAAGGGCATCTGGATC 2220
QY 653 ----- 653
DB 2221 CCTGATGGGGAGAAATGTGAAATTTCCAGTGGCCATCAAAAGTGTGAGGAAACACATCC 2280
QY 653 ----- 653
DB 2281 CCCAAAGCCAAAGAAATCTTAGCAAGCATACGTGATGGCTGTGTGGCTCTCCCA 2340
QY 653 ----- 653
DB 2341 TATGTCTCCCGCTTCTGGGCATCTGCTGACATCCAGGTGCAGCTGTGTGACACAGCTT 2400
QY 653 ----- 653
DB 2401 ATGCCCTATGGCTGCTCTTAGACCATGTCCGGGAAACCCGCGAGCGCTGGGCTCCAG 2460
QY 653 ----- 653
DB 2461 GACCTGTGAATCTGGTGTATGATGATTTGCCAAGGGGATGAGCTACCTGGAGAGTGTGCGG 2520
QY 653 ----- 653
DB 2521 CTGTGACACAGGAGCTTTGGCCCTCGGAACTGTGCTGCAAGCTGTGCTCAAGAGTCCCAACATGTCAA 2580
QY 653 ----- 653
DB 2581 ATTACAGACTTGGGGCTGGCTCGGCTGTGCAATTCACGAGACAGAGTACCATGCAGAT 2640
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DB 2641 GGGGCAAGTGTGCCATCAAGTGTGATGCGCTGTGATGCTCATTTCTCCGCCGGGTTCACC 2700
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DB 2701 CACCAGAGTGTGTGTGAGTGTATGTGTGTGATGTGTGTGGAGCTGTATGACTTTTGGGGCC 2760
QY 653 ----- 653
DB 2761 AAACCTTACGNTGGATCCAGCCCGGAGATCCCTGACCTGTGGAAGGGGGAGCGG 2820
QY 653 ----- 653
DB 2821 CTGCCCCAGCCCCCATCTGCACCATGTATGTCTACATGATCATGTGTGTCAAATGTTGATG 2880
QY 653 ----- 653
DB 2881 ATTGACTCTGAATGTTCGGCCAGATTCCTGGAGTGTGTGTGTAATTTCTCCCGCATGGCC 2940
QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
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Db 2941 AGGACCCCCAGCGCTTTGTGTTCATCCAGAAATGAGGACTTGGGCCCCAGCCAGTCCCTTG 3000
 Qy 665 AppSerThrPheTyrArgSerLeuLeuGluAspMetGlyAspLeuValAspAla 684
 Db 3001 GACAGCCTTCTACCGCTCACTGCTGAGGAGCATGATGGGGACCTTGTGGATGCT 3060
 Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
 Db 3061 GAGGAGTATCTGTACCCAGCAGCGGCTTCTTCTGTCCAGACCCCTGCCCCCGGCGCTGG 3120
 Qy 705 GlyMetValHisHisArgHisArg 712
 Db 3121 GGCATGGTCCACACAGGACCCG 3144

RESULT 7
 US-10-280-576-3
 ; Sequence 3, Application US/10280576
 ; Publication No. US20040044405A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wolff, Matthew R.
 ; TITLE OF INVENTION: VASCULAR STENT OR GRAFT COATED OR IMPREGNATED WITH PROTEIN
 ; FILE REFERENCE: 09820.189
 ; CURRENT APPLICATION NUMBER: US/10/280,576
 ; CURRENT FILING DATE: 2002-10-22
 ; PRIOR APPLICATION NUMBER: 60/343,732
 ; PRIOR FILING DATE: 2001-10-25
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 3768
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-280-576-3

Alignment Scores:
 Pred. No.: 0 Length: 3768
 Score: 3776.00 Matches: 712
 Percent Similarity: 67.94% Conservative: 0
 Best Local Similarity: 67.94% Mismatches: 0
 Query Match: 95.50% Indels: 336
 DB: 13 Gaps: 1

US-09-493-480-7 (1-712) x US-10-280-576-3 (1-3768)

Qy 1 MetGluLeuAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
 Db 1 ATGGAGTGGCGGCTTGTGGCGCTGGGGCTCTCTGCGCTCTTGGCCCCCGAGCC 60
 Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
 Db 61 GCGAGCACCAGTGTGCACCGSCACAGACATGAAGCTGCGGCTCCCTGCCAGTCCCGAG 120
 Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
 Db 121 ACCCACTGGATGCTCCGCCACCTCTACAGGGCTGCGAGTGTGCGGGAACCTG 180
 Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
 Db 181 GAACCTACCTACCTGCCACCAATGCGAGCTGCTCTCTGCGAGTATCCAGGAGGTG 240
 Qy 81 GlnGlyTyrValLeuLeuAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
 Db 241 CAGGGCTAGCTGCTATCGCTCACACCAAGTGGAGCGAGTCCCACTGCGAGAGGCTGGG 300
 Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
 Db 301 ATTGTGCGAGGACCCAGCTCTTTTGGAGCAACTATGCCCCCTGGCCCTGTAGCAATGGA 360
 Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
 Db 361 GACCCGCTGACATACCACTCCCTGTCCAGGGGCTCCCGAGGAGCTGGCGAGCTG 420
 Qy 141 GlnLeuArgSerLeuThrGluLeuLeuLysGlyValLeuLeuLeuLeuLeuLeuLeuLeu 160
 Db 421 CAGCTTCGAGCCCTCACAGAGATCTTGAAGAGGGTCTTGAATCAGCGGAACCCCCAG 480
 Qy 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnGlnLeuAla 180
 Db 481 CTCTGCTACAGGACACGANTTTGTGGAAGGACATCTTCCACAAGAACCAACAGCTGGCT 540
 Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
 Db 541 CTCACATGATAGACACCAACGCTCTCGGGCTCCCACTGCTGCTGCTGCTGCTGCTGCTG 600
 Qy 201 GlySerArgCysTrpGlyLysSerGluAspCysGlnSerLeuThrArgThrValCys 220
 Db 601 GCTCCCTGCTGCTGGGAGAGATTTCTGAGAGATTTCTGAGAGCTGACGGCCTGCTGCTG 660
 Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
 Db 661 GCGGCTGCTGCTGCCGCTGCAAGGGCCACTGCTGCCACTGACTGCTGCCATGAGCAGTGT 720
 Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
 Db 721 GCTGCGGCTGCAAGGGCCCAAGCACTCTGACTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
 Db 781 AGTGGCATCTGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 Qy 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
 Db 841 TCCATGCCCATCCCGAGGCGGTATACATTCGGGGCCAGCTGTGTGCTGCTGCTGCTGCT 900
 Qy 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
 Db 901 TACAACTACTTCTACGAGCTGGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
 Db 961 GAGGTGACAGCAGAGGTGGAACACAGCGTGTGAGAGTGGAGAGGCTTGTGCTGCTGCTG 1020
 Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
 Db 1021 GTGTGCTATGCTGCGGCAATGAGCACTTTCGAGAGGTGAGGGCAGTTACCAAGTGTTC 1080
 Qy 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
 Db 1081 ATCCAGAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
 Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnValPhe 400
 Db 1141 TTTGATGGGACCCAGCTTCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 Qy 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaIleProAspSerLeuPro 420
 Db 1201 GAGACTCTGGAAGAGATCACAGTTACCTATATACATCTCAGCATGGCGGAGCAGCTGCT 1260
 Qy 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
 Db 1261 GACCTCAGGCTTTCAGAACTGCAAGTAATCCGGGAGCAATTCCTGCAAAATGGCGCC 1320
 Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuArgSerLeuArgGlu 460
 Db 1321 TACTGCTGACCTGCGAGGCTGGGCATCAGCTGCTGGGGCTGGCTGCTGCTGCTGCTGCTG 1380
 Qy 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
 Db 1381 CTGGGCACTGGAGCTGGCCCTCATCCACCATAAACCCACCTGCTGCTGCTGCTGCTGCTG 1440
 Qy 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
 Db 1441 CCTTGGGACAGCTCTTTTGGAAACCCGACCAAGCTCTGCTGCTGCTGCTGCTGCTGCTG 1500
 Qy 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520

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Db 1501 GAGGACGAGTGTGGGCGAGGCGCTGGCCCTGCCACACGAGCTGTGGCGCCGAGGCGACTGC 1560
Qy 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Db 1561 TGGGGTCCAGGGCCACCCAGTGTGTCAACTGCGAGCCAGTTCTTCTGGGGCCAGGAGTGC 1620
Qy 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTrpValAsnAlaArgHisCys 560
Db 1621 GTGGAGGAATGCCGAGTACTGCGAGGGCTCCCGAGGGAGTATGTGAATGCCAGGCACTGT 1680
Qy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 1681 TTCCCGTGCACCCCTGAGTGTGACGCCAGCAATGGCTCAGTGACCTGTTTGTGACCGGAG 1740
Qy 581 AlaAspGlnCysValAlaCysAlaHisTrpLysAspProPheCysValAlaArgCys 600
Db 1741 GCTGACCAAGTGTGGCCTGTGCCCACTAAGAGCCCTCCCTTCTGCGTGGCCGCGTGC 1800
Qy 601 ProSerGlyValLysProAspLeuSerTrpMetProIleTrpLysPheProAspGluGlu 620
Db 1801 CCAGCGGTGTGAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG 1860
Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
Db 1861 GGGCGATGCCAGCCTTGGCCCATCACTGCACCCACTCTCTGTGTGACCTTGGATGACAG 1920
Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
Db 1921 GGCTGCCCGCGAGCAGAGCCAGCCCTCTGAGGTCCATCTGCGGTGGTTGGC 1980
Qy 653 653
Db 1981 ATTCTGCTGCTGCTGTGGTCTTGGGGTGGTCTTTTGGGATCCTCATAGCGACGCGAGCAG 2040
Qy 653 653
Db 2041 AGATCCGGAAGTACAGATGCGGAGACTCTCTGAGGAACGAGCTGTGGTGGACCGCTG 2100
Qy 653 653
Db 2101 ACACCTAGCGGAGGATGCCAACACAGCGCGAGATCGGATCCTGAAAGAGACGAGCTG 2160
Qy 653 653
Db 2161 AGGAAGTGAAGTGTCTGTGATCTGGCGCTTTTGGCACTCTACAGGCGATCTGGATC 2220
Qy 653 653
Db 2221 CCTGATGGGGAGAAATGTGAAAAATTCAGTGGCCATCAAAGTGTGAGGGAAACACATCC 2280
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Db 2281 CCCAAGCCAAACAAAGAAATCTTTAGACGAAGCATACGTGATGGTGTGGGCTCCCA 2340
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Db 2341 TATGTCTCCGCGCTTCTGGGCATCTGCTTGACATCCACGGTGCAGCTGTGACACAGCTT 2400
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Db 2401 ATGCCCTATGGCTCTCTTAGACCATGTCCGGGAACCGCGGAGCGCTGGGCTCCAG 2460
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Db 2521 CTGCTACACAGGACTTGGCGCGCTCGGAAGCTGTGCTCAAGAGTCCCAACCATGTCAAA 2580
Qy 653 653
Db 2581 ATTACAGACTTGGGGTGGCTCGGCTGTGGAATTTGACGAGACAGAGTACCATGACAGAT 2640
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Db 2641 GGGGGCAAGTGGCCCATCAAGTGGATGGCGCTGGAATCCATTCTCCGCCGCGGGTTCCACC 2700
Qy 653 653
Db 2701 CACCAGAGTATGTGTGGAGTTATGGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGGCC 2760
Qy 653 653
Db 2761 AAACCTTACGATGGGATCCCGAGCCCGGAGATCCTTGACCTGTCTGAAAAAGGGGAGCGG 2820
Qy 653 653
Db 2821 CTGCCCCAGCCCCCATCTGACCATTTGATGTCTACATGATCATGTGTCAAATTTGGATG 2880
Qy 653 653
Db 2881 ATTGACTCTGAATGTCCGCCAAGATTCGGGAGTTGGTGTCTGAATTTCTCCGCGATGGCC 2940
Qy 654 654
Db 2941 AGGAGCCCCCAGCGCTTTGTGGTCAATCCAGATCAGGACTTTGGGCCAGCCAGTCCCTTG 3000
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Db 3001 GACAGCACCTTCTACCGCTCACTGCTGGAGACGATGACATGGGGGACCTGTGTGATGCT 3060
Qy 685 GluGluTrpLeuValProGlnGlnGlyPheCysProAspProAlaProGlyValaGly 704
Db 3061 GAGAGTATCTGGTACCCCGAGCGGCTTCTTCTGTCCAGACCTTGCCCCGGCGCTGGG 3120
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RESULT 8

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US-09-765-973-1
; Sequence 1, Application US/09765973
; Publication No. US20020039573A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Hand-Zimmermann, Susan
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR PREVENTION AND
; TITLE OF INVENTION: TREATMENT OF HER-2/neu ASSOCIATED MALIGNANCIES
; FILE REFERENCE: 210121.496
; CURRENT APPLICATION NUMBER: US/09/765,973
; CURRENT FILING DATE: 2001-01-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-09-765-973-1
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Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 13 Gaps: 1
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US-09-493-480-7 (1-712) x US-09-765-973-1 (1-3768)

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Db 1 ATGAGACTGGCGGCTTGTGCCGCTGGGGGCTCTCTCTGCGCCCTTTCGCCCGGAGCC 60
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Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 61 GGGAGCAACCAAGTGTGACCGGCACACAGATGAAGCTGGGCTCCCTGCCAGTCCCGAG 120
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlnLeu 60
Db 121 ACCCACTGGACATGCTCCGCCACCTCTACCAAGGGCTGCGAGGTGGTGCAGGAAACCTG 180
Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 181 GAACCTCAGCTACCTGCCACCAATGCCAGCCCTGTCTCTCTGCAGATATCCAGAGGTG 240
Qy 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 CAGGGCTACGTGCTCATCGCTCACAAACCAAGTGAGCGAGGTCCCACTGCAGAGGCTGGG 300
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 301 ATTGTGCGAGGCAACCGAGCTCTTTGAGGACAACTATGCTCCCTGGCCGTGTGATGCAATGGA 360
Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 361 GACCCGCTGAAACAATACCAACCCCTGTACAGGGGCTCCCAAGAGGCTGCGGGAGCTG 420
Qy 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 421 CAGCTTCGAGAGCTCACAGATCTTGAAAGGAGGGGTCTTGATCCAGCGGAACCCCGAG 480
Qy 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 481 CTCTGCTACAGGACACGATTTGTGGAAGGACATCTTCCACAGAAACAACAGCTGGCT 540
Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 541 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCGCCCTGTCTCCGATGTGAAG 500
Qy 201 GlySerArgCysTyrGlyLeuSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 601 GACTCCCGCTGTGGGAGAGAGTCTTGAGGATTTGTACAGAGCTGACGGCGACTGTCTGT 660
Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
Db 661 GCGCGTGGCTGTGCGCGCTGCAAGGGGCCACTGCCCACTGACTGCTGCCATGACGAGTGT 720
Qy 241 AlaIleGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 721 GCTGCCGCTGACAGGGCCCCAAGCACTCTGACTGCTTGGCTGGCTCCACTTCAACACAC 780
Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 781 AGTGGCATCTGTGAGCTGCACTGCCCGAGCCCTGCTCACCAACACAGACAGCTTTGAG 840
Qy 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 841 TCCATGCCCAATCCCGAGGCGCGGTATACATTCGGGCGCCAGCTGTGTGACTGCTGTCCC 900
Qy 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db 901 TACAACCTACTTTCTACGGAGCGTGGATCTTGACCCCTGTGTGCTGCCCTTGCAACACCA 960
Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
Db 961 GAGGTGACAGCAGAGGATGGAAACACAGCGGTGTGAGAGTGCAGCAAGCCCTGTGCCCGA 1020
Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
Db 1021 GTGTGCTATGGTCTGGGCAATGGAGCACTTTCGAGAGGTGAGGGCAGTTACAGTGCCTAAT 1080
Qy 361 IleGlnGluPheAlaGlyCysValValIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 1081 ATCCAGAGGTTTCTGGCTGCAAGAGATCTTTGGGAGGCTTGCAATTTCTGCCGGAGAGC 1140

Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
Db 1141 TTTGATGGGACCCAGCCTCCAACTGCCCCGCTCCAGCCAGAGAGCTCCAAAGTGT 1200
Qy 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420
Db 1201 GAGACTCTGGAAGAGATCACAGTTTACCTATACATCTCAGCATGCGCGACAGCTGCCT 1260
Qy 421 AspLeuSerValPheGlnAsnLeuGlnValIleLeuArgIleLeuHisAsnGlyAla 440
Db 1261 GACCTCAGCGCTCTTCAGAACCTGCAAGTAAATCCGGGACGAATCTTGCAACAATGGCC 1320
Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuGlyLeuArgSerLeuArgGlu 460
Db 1321 TACTCGCTGACCTTCGAAGGGCTGGGCATCAGCTGGCTGGGGCTGGCGCTCAGTGAAGGA 1380
Qy 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
Db 1381 CTGGGAGTGGACTGGCCCTCATCCACATTAACACCCACTCTGCTTCGTGACACAGGTG 1440
Qy 481 ProTyrAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
Db 1441 CCTTGGGACCACTCTTTCGGAACCGCACCAAGCTCTGCTCCACACTGCAACCCGCGCA 1500
Qy 501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
Db 1501 GAGGACGAGTGTGGGGGAGGGCTGGCTTCCACACGCTGTCGCCCGCGAGGGCACTGC 1560
Qy 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Db 1561 TGGGTTCAGGGCCCAACCCAGTGTCTCACTGACGACAGTTCCTTTCGGGGCCAGAGTGC 1620
Qy 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
Db 1621 GTGGAGGAATGCCAGTACTGACGGGCTCCCGAGGAGTATGTGAATGACGACACTGT 1680
Qy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 1681 TTGCGCGTGCACCTTGTAGTGTGAGCCCAAGATGGCTCAGTGACCTGTTTGGACCGGAG 1740
Qy 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600
Db 1741 GCTGACCACTGTGTGGCTGTGCCCACTATAGGACCTCTCCCTTCTGGTGGCGCGCTGC 1800
Qy 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu 620
Db 1801 CCCAGCGGTGAAACCTGACCTCTCTACATGCCCATCTGGAAGTTCAGATGAGGAG 1860
Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
Db 1861 GGGCGCATGCCAGCTTGGCCCCATCAACTGACCACTCTCTGTGTGGACCTGGATGACAG 1920
Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
Db 1921 GACTGCCCGCGCAGGAGGAGGACGACCCCTCTGACCTCCATCTCTCGGCTGGTGGC 1980
Qy 653 653 653
Db 1981 ATTCTGCTGTGTGTGTGGGTGCTTGGGGTGGTCTTTGGGATCTCTCATAGCGACCGACAG 2040
Qy 653 653 653
Db 2041 AAGATCCGGAAGTACACGATGGGAGACTGCTGCCAGGAACCGGAGCTGTGTGGAGCCGCTG 2100
Qy 653 653 653
Db 2101 ACACCTAGCGGAGGATGCCCAACCGAGCGCAGATGGGATCTCTGAAGAGAGACGAGAGCTG 2160
Qy 653 653 653
Db 2161 AGGAAGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTTACAAGGCACTCTGTGATC 2220
Qy 653 653 653


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Db 2221 CCTGATGGGAGAAATGTGAAATTCAGTGGCCATCAAGTGTAGGGAAAAACACATCC 2280
Qy 653 -----
Db 2281 CCCAAAGCCAAAGAAATCTTAGAGGAAGCATACGTGATGGCTGTGGGTCCCA 2340
Qy 653 -----
Db 2341 TATGTCTCCGCTCTCTGGGCAATCTGCTGACATCCAGCGTGACAGTGTGACACAGCTT 2400
Qy 653 -----
Db 2401 ATGCCCTATGGCTCTCTTAGACCATGTCTCGGGAACCGCGACGCTGGGCTCCAG 2460
Qy 653 -----
Db 2461 GACCTGTGAACCTGTGTATGAGATTGCCAAGGGATGAGCTACCTGGAGGATGTGGG 2520
Qy 653 -----
Db 2521 CTGTACACAGGACTTGGCGCTCGGAACGTGCTGTCAAGTCTCCCAACCATGTCAA 2580
Qy 653 -----
Db 2581 ATTACAGACTTGGGCTGGCTCGGCTGTGACATTTGACGAGACAGAGTACCATGCAGAT 2640
Qy 653 -----
Db 2641 GGGGCAAGTGCCCATCAAGATGAGTGGCTGAGTGCCATTTCTCCCGCGGCTTCCAC 2700
Qy 653 -----
Db 2701 CACCAGAGTATGTGTGAGTTATGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCC 2760
Qy 653 -----
Db 2761 AAACCTTACGATGGATCCAGCCCGGAGATCCCTGACCTGTCTGGAAGGGGGAGCGG 2820
Qy 653 -----
Db 2821 CTGCCCCAGCCCCCATCTGCACCATTTGATGATCTACATGATCATGGTCAATGTGGATG 2880
Qy 653 -----
Db 2881 ATTGACTCTGAATGTGCGCAAGATTCGGGAGTTGGTGTCTGAATTTCTCCGCGATGCC 2940
Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProIleu 664
Db 2941 AGGACCCCCAGCCCTTTGTGTCATCCAGAAATGAGGACTTGGGCCCCAGCCAGTCCCTTG 3000
Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGACCTTTCTACCCGCTCACTGTGAGAGACATGATGAGGGGAGCTGGTGGATGCT 3060
Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyValaGly 704
Db 3061 GAGAGTATCTGGTACCCAGCAGGGCTTCTTCTGTCAGACCCCTGCCCCGGCGCTGGG 3120
Qy 705 GlyMetValHisHisArgHisArg 712
Db 3121 GGCGATGTCACACAGGACCGC 3144
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RESULT 9

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US-10-313-644-1
; Sequence 1, Application US/10313644
; Publication No. US20030157119A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: Hand-Zimmerman, Susan
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL
; TITLE OF INVENTION: AND VIRUS-ASSOCIATED MALIGNANCIES
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; FILE REFERENCE: 210121.483C3
; CURRENT APPLICATION NUMBER: US/10/313,644
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
; US-10-313-644-1
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Alignment Scores:

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Pred. No.: 0 Length: 3768
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 15 Gaps: 1
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US-09-493-480-7 (1-712) x US-10-313-644-1 (1-3768)

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Qy 1 MetGluLeuAlaLeuCysArgTyrGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
Db 1 ATGGAGCTGGCGGCTTTGTGCGCTGGGGCTCTCTCGCCCTTTGCCCTTTCCTCCCGGAGCC 60
Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLeuLeuArgLeuProAlaSerProGlu 40
Db 61 GCGAGACCCCAAGTGTGACCGCACAGACATGAGCTGCGGCTCCCTGCCAGTCCCGAG 120
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 121 ACCCACCTGGACATGCTCGCCACCTCTTACCGAGGCTGCCAGGTGGTGCAGGGAACCTG 180
Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
Db 181 GAATCCTACCTACCTGCGCCCAATGCCAGCTGCTCTTCTCCAGGATATCCAGGAGGTG 240
Qy 81 GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 CAGGGCTAGCTGCTCATGCTCACAACCAAGTAGGAGGAGTCCCACTGCAGAGGCTGGCG 300
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 301 ATTGTGCGAGGACCCAGCTCTTTGAGGACAATATGCGCTGGCGTGTCTACACAATGGA 360
Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 361 GACCCGCTGAACAATACCAACCCCTGTCAAGGGGCTCCCGAGGAGGCTTCCGGAGCTG 420
Qy 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 421 CAGCTTCGAACCTTCACAGAGATCTTGAAGAGAGGGGTCTTGATCCAGCGGAAACCCCA 480
Qy 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 481 CTCTGCTACCAAGACACGATTTTGTGGAAGGACATCTTCCACAAGACAACACAGCTGGCT 540
Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 541 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTCCGATGTGTAG 600
Qy 201 GlySerArgCysTyrGlyLeuSerSerGluLeuSerGlnSerLeuThrArgThrValCys 220
Db 601 GGCTCCCTGCTGTGGGAGAGATTTCTGAGGATTTCTAGAGCTTCTAGCGCTGACCGGCTGTCT 660
Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
Db 661 GCGGCTGCTGTGCGGCTGCAAGGGGCCACTGCCCACTGACTGCTGCTGCCATGAGCAGTGT 720
Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
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Db	721	GCTGCGGCTGCACGGGCCCCAAGCACTCTGACTGCTGGCTGCTCCACTTCAACCAAC	780	Db	1801	CCCAGCGGTGTAACCTGACCTCTCTACATGCCCATCTGGAGTTTCCAGATGAGGAG	1860
Qy	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280	Qy	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640
Db	781	AGTGGCATCTGTGAGCTGCACCTGCCAGCCCTGGTCACTCAACACACAGACAGCTTTGAG	840	Db	1861	GGCGCATGCCAGCTTTGCCCATCAACTGCACCCACTCTCTGTGTGGACCTGGATGACAAG	1920
Qy	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300	Qy	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
Db	841	TCCATGCCAATCCCGAGGGCCGGTATACATTCGGCGCCAGCTGTGTGACTGCTGTCC	900	Db	1921	GGCTGCCCGCCGCGAGAGAGAGCCAGCCCTCTGACGTCCATCATCTCTGCGGTGGTTGGC	1980
Qy	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320	Qy	653	-----	653
Db	901	TACAACTACCTTTCTACGAGCTGGATCTCTGACCTCTGCTGCCCTGCACAACCAA	960	Db	1981	ATTCTGCTGCTCGTGGTCTTGGGGGTGGTCTTTTGGGATCCTCATCAAGCGACCGCAGCAG	2040
Qy	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340	Qy	653	-----	653
Db	961	GAGGTGACAGCAGAGATGGAAACACAGCGGTGTGAGAGTGCAGCAAGCCCTGTGCCGA	1020	Db	2041	AGATCCCGAGTACACGATGCGGAGACTGCTGCAGGAAACCGGAGCTGGTGGAGCCGCTG	2100
Qy	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360	Qy	653	-----	653
Db	1021	GTGTCTATFGTCTGGGATGAGGACCTTGCAGAGGTGAGGGCAGTTACCACTGCCAAT	1080	Db	2101	ACACCTAGCGGAGCGATGCCAACACGAGCGCAGATGCGGATCCTGMAAGAGACGGAGCTG	2160
Qy	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380	Qy	653	-----	653
Db	1081	ATCCAGGAGTTTGTCTGGCTGCAAGAAGATCTTTGGGAGCTGGCATTTCTGCCGGAGAGC	1140	Db	2161	AGGAAGTGAAGGTGCTTGGATCTGGCGCTTTTGGGCACAGTCTTACAAGGGCATCTGGATC	2220
Qy	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluLeuGlnValPhe	400	Qy	653	-----	653
Db	1141	TTTGTATGGGGACCCAGCCCTCCAACTGCCCCGCTCCAGCCAGAGAGCTCCAAAGTGT	1200	Db	2221	CCTGATGGGAGATGTGAANAATTCAGTGGCCATCAAAAGTGTGTAGGGAAAAACACATCC	2280
Qy	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro	420	Qy	653	-----	653
Db	1201	GAGACTCTGGAAGAGATCACAGTTACCTATACATCTCAGCATGGCCGAGACGCTGCT	1260	Db	2281	CCCCAAGCCCAACAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA	2340
Qy	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440	Qy	653	-----	653
Db	1261	GACCTCAGCGTCTTCAGAACTGCAAGTAATCCGGGGACGAATCTGCACAAATGGCGCC	1320	Db	2341	TATGTCTCCCGCTTCTGGGCATCTGCCCTGACATCCACGGTGCAGCTGGTGACACAGCTT	2400
Qy	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuGlyLeuArgSerLeuArgGlu	460	Qy	653	-----	653
Db	1321	TACTGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGGCTCCTCCTGAGGAA	1380	Db	2401	ATGCCCTATGCTGCTCTTAGACCATGTCCGGGAAAAACCGCGAGCCCTGGGCTCCCAG	2460
Qy	461	LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal	480	Qy	653	-----	653
Db	1381	CTGGGCGATGGACTGGCCCTCATCCACATACACCCACTCTGCTTCTGTGCACACGGTG	1440	Db	2461	GACCTGCTGAATGCTGTGTATGAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGGG	2520
Qy	481	ProTyrAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500	Qy	653	-----	653
Db	1441	CCCTGGGACCACTCTTCGGAACCCGCAACCAAGCTCTGCTCCACACTGCCAACCGGCCA	1500	Db	2521	CTCGTACACAGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAA	2580
Qy	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520	Qy	653	-----	653
Db	1501	GAGGACAGTGTGTGGGCGAGGGCTTGGGCTGCGCACAGCTGTGGCCCGAGGGCACTGC	1560	Db	2581	ATTACAGACTTCGGGCTGGCTGGCTGGACATTTGACGAGACAGAGTACCATGCAAGAT	2640
Qy	521	TyrGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540	Qy	653	-----	653
Db	1561	TGGGTCCAGGGCCCAACAGTGTGTCAACTGACGACCAAGTTCTTCTGGGGCCAGGAGTGC	1620	Db	2641	GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTGCATTCTCCGCCCGCGGTTCACC	2700
Qy	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560	Qy	653	-----	653
Db	1621	GTGGAGGAATGCCAGTACTGCAGGGGCTCCCGAGGAGTATGTGAATGCCAGGCACTGT	1680	Db	2701	CACCAGATGATGTGTGGAGTTATGGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC	2760
Qy	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580	Qy	653	-----	653
Db	1681	TTGCCGTGCCCTCTGAGTGTGAGCCCAAGATGGCTCAGTGACCTGTTTGGACGGGAG	1740	Db	2761	AAACCTTACGATGGGATCCAGGCCCGGAGATCCCTGACCTGTCTGGAAGGGGGAGCGG	2820
Qy	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys	600	Qy	653	-----	653
Db	1741	GCTGACCAGTGTGGCTGTGCCACTATAGGACCCCTCCCTTCTGCGTGGCCCGCTGC	1800	Db	2821	CTGCCCAAGCCCCCATCTGACCACTTGTATGATGTCTACATGATCATGTGTCAAATGTTGATG	2880
Qy	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu	620	Qy	653	-----	653
Db				Db	2881	ATTGACTCTGAATGTCCGGCAAGATTCGGGGAGTTGGTGTCTGAATTCCTCCCGCATGGCC	2940

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Qy 654 -----GlnAenGluAsePLeuGlyProAlaSerProLeu 664
Db 2941 AGGACCCCCAGCGCTTTGTGCTCATCCAGAAATGAGGACTTGGGCCCCAGCGAGTCCCTTG 3000
Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAsePLeuMetGlyAspLeuValAseAla 684
Db 3001 GACAGCACTTCTACCGCTCACTGCTGGAGGACCATGACATGGGGGACCTGGTGATGCT 3060
Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGGTACCCAGCAGGCTTCTTCTGTCCAGACCTTGCCCGGGCGCTGGG 3120
Qy 705 GlyMetValHisHisArgHisArg 712
Db 3121 GGCATGTGTCCACCACAGGACCCG 3144

RESULT 10
US-09-441-411-5
; Sequence 5, Application US/09441411
; Publication No. US2003008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-441-411-5

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 336
Query Match: 95.50% Indels: 1
DB: 10 Gaps: 1

US-09-493-480-7 (1-712) x US-09-441-411-5 (1-4473)
Qy 1 MetGluLeuAlaLeuCysArgTTPGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
Db 175 ATGGAGCTGGCGGCTTTGTGCGCTGGGGGCTCCTCTCGCCCTTTGCCCGCCGAGCC 234
Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 235 GCGAGCACCCAAAGTGTGACCGGCACAGCATGAGCTGCGGCTCCCTGCCGAGTCCCGAG 294
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 295 ACCCACTGGNACATGCTCCGCCACTCTACCGAGGCTGCCAGGTGGTGCGAGGAAACCTG 354
Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 355 GAACTACCTACCTGCCCAACCAATGCCAGCGCTGCTTCTTCGACGATATCCAGAGGTG 414
Qy 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 415 CAGGGCTACGTCGTCATGCTCACAACCAAGTGGGAGGCTCCCACTGCAGAGGCTCGCG 474
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 475 ATTGTGGAGGACCCAGCTCTTTGAGGACCACTATGCCCTGGCGGTGCTAGACAATGGA 534
Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140

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Db 535 GACCGCTGAACAATACCAACCCCTGTCAAGGGGCTTCCCCAGAGGCTTGGCGGAGCTG 594
Qy 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln 160
Db 595 CAGCTTCGAGGCTCACAGAGATCTTGAAGGAGGGGTCTTGATCCAGCGGAACCCCGAG 654
Qy 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisIleAsnGlnLeuAla 180
Db 655 CTCTGCTACCAAGGACAGCATTTTGTGGAAGGACATCTTCCACAAGAACAACCAAGCTGGCT 714
Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisIleProCysSerProMetCysLys 200
Db 715 CTCACACTGATAGACCAACCGCTCTCGGGCTTCCACCCCTGTCTCCGATGTGTAG 774
Qy 201 GlySerArgCysTrpGlySerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 775 GGCTCCCGCTGCTGGGGAGAGAGTTCTGAGGATTTGTACAGGCTTGCAGCGGCTGTCTGT 834
Qy 221 AlaGlyCysAlaArgCysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
Db 835 GCGGTGCTGTGCGCGCTGCAAGGGGCACTGCCCACTGACTGCTGCCATGAGCAGTGT 894
Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 895 GCTGCGGCTGCACGGGCCCCAAGCACTCTGACTGCTGGCTGGCTCCACTTCAACCCAC 954
Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 955 AGTGCACTGTGAGTGCACCTGCCAGCCCTGGTCACTACACACACAGCAGTTTGAG 1014
Qy 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 1015 TCCATGCCCAATCCGAGGCGCGGTATACATTTGGCGGCGAGCTGTGTGAGCTGCTGCC 1074
Qy 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db 1075 TACAACCTACCTTTCTACGGAAGTGGGATCTTGGAGCTTGTGACCTGCTGCCCTTGCACAAACCAA 1134
Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
Db 1135 GAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAGTGCAGCAAGCCCTGTGCCCGA 1194
Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
Db 1195 GTGTGCTATGCTTGGGCATGAGCACTTGCAGAGGTGAGGGCAGTTACCAAGTGCAT 1254
Qy 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 1255 ATCCAGGAGTTGTCTGGCTGCAAGAGATCTTGGGAGCTTGGCATTTCTCCGGAGAGC 1314
Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe 400
Db 1315 TTTGATGGGACCCAGCTCCCAACACTGCCCGCTCCAGCCAGCAGCAGCTCCCAAGTGT 1374
Qy 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
Db 1375 GAGACTCTGGAAGAGATCACAGGTTTACCTATATCATCTCAGCATGCGCGAGCCTGCT 1434
Qy 421 AsnLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisGlnGlyAla 440
Db 1435 GACTCAGCGTCTTCCAGAACCTGCAAGTAAATCCGGGAGCGAATTTCTGCACATGCGCC 1494
Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
Db 1495 TACTGCTGACCTTGCAGAGGCTGGGCATCAGCTGGCTGGGGCTGGCTCCTACTGAGGAA 1554
Qy 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
Db 1555 CTGGGAGTGAGCTGGGCTCTCATCCACATAACACCCACTCTGCTGTGTCACACGGTG 1614
Qy 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500

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Db	1615	CCCTGGGAC	CAGCTCTTTTCGGAA	CCCGGCA	CCAAAGCTCTGCTCCACACTGCTCCACACCGCGCCA	1677
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Db	1675	GAGGACGAGTGTGTGGCGAGGGCTGGCTGGCCACCA	CCAGCTGTGTGGCCGCGAGGCACTGC	1734		
Qy	521	TrpGly	ProGly	ProThr	GlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
Db	1735	TGGGGTCCAGGGGCCAC	CCAGTGTCTCACTGCAGCCAGTTCCTTCTGGGGCCAGGAGTGC	1794		
Qy	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560			
Db	1795	GTGGAGAAATGCCAGTACTGCAGGGGCTCC	CCAGGAGTATGTGAATGCCAGGACTGT	1854		
Qy	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580			
Db	1855	TTGGCGTGCCACCTTGAGTGT	CAGCCAGAAATGGCTCACTGACCTGTGTTCGACCGGAG	1914		
Qy	581	AlaAspGlnCysValAlaCysAlaHisTyrIysAspProProPheCysValAlaArgCys	600			
Db	1915	GCTGACCAGTGTGTGGGCTGTGGCCACTATAAGAGACCTCCCTCTTCTGCGTGGGCCGCTGC	1974			
Qy	601	ProSerGlyValIysProAspLeuSerTyrMetProIleThrIysPheProAspGluGlu	620			
Db	1975	CCCAAGCGGTGGAACCTGACCTCTCTCTACATGCCCATCTGGAGATTTCCAGATGAGGAG	2034			
Qy	621	GlyValaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspIys	640			
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Qy	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653			
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RESULT 11

RESULTS 11
US-10-146-473-32
: Sequence 32. Application US/10146473

; Publication No. US20
: GENERAL INFORMATION:

APPLICANT: Scanlan, Ma
APPLICANT: Gout, Ivan

APPLICANT: Stockert, Ali
APPLICANT: Gure, Ali

APPLICANT: Chen, Yao-
APPLICANT: Old, Lloyd

; TITLE OF INVENTION: Breast Cancer Antigens
 ; FILE REFERENCE: L00461/70130(JRV)

; CURRENT APPLICATION NUMBER: US/1
 ; CURRENT FILING DATE: 2002-05-15

; PRIOR APPLICATION NUMBER: US 60/291,150
 ;
 ; PRIOR FILING DATE: 2001-05-15

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; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn version 3.0.0

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; SEQ ID NO 32
; LENGTH: 4473

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; TYPE: DNA
; ORGANISM: Homo sapiens

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Alignment Scores:

Alignment Scores:			
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Score:	3776.00	Matches:	712
Percent Similarity:	67.94%	Conservative:	0
Best Local Similarity:	67.94%	Mismatches:	336
Query Match:	95.50%	Indels:	15
DB:	15	Gaps:	1

US-09-493-480-7 (1-712) x US-10-146-473-32 (1-4473)

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QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
DB 235 GCGAGCACCCAGTGTGTGACCGGCACAGACATGAGCTGGGGCTCCCTGCGCAGTCCCGAG 294
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrglnGlyCysGlnValValGlnGlyAsnLeu 60
DB 295 ACCACCTGGACATGCTCCGCCACCTCTACAGGGCTGCCAGGTGGTGGAGGAACCTG 354
QY 61 GluLeuThrThrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
DB 355 GAACCTACCTACCTGCCCCACCATGCGAGCTGTCTCTCTGAGGATATCCAGGAGGTG 414
QY 81 GlnGlyTyrrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
DB 415 CAGGGCTACGTGCTCATCGCTCAACACCAAGTGGGAGGCTCCCACTGCGAGAGCTGGCG 474
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
DB 475 ATTGTGCGAGGCCACCCAGCTCTTTGAGGACAACTATGCTCCCTGGCCGTGTAGCAATGGA 534
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
DB 535 GACCCCTGAAACAAATACCACTCTGTCAAGGGGCTCCCGAGAGGCTCGGGAGCTG 594
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
DB 595 CAGCTTCGAAGCTTCACAGAGATCTTTGAAGAGGGGTCTTGATCCAGCGGAACCCCGAG 654
QY 161 LeuCysTyrrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
DB 655 CTCTGCTACAGACACGATTTTGTGAAGGACATCTTCACAAAGAACCAACAGCTGGCT 714
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
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QY 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
DB 775 GGCTCCCGCTGCTGGGAGAGATCTCTGAGATTGTTCAGAGCTGACGCGCACTGTCTGT 834
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
DB 835 GCGGTGGCTGTGCCCGCTGCAAGGGGCCACTGCCCACTGCTGCTGCCATGAGCAGTGT 894
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
DB 895 GCTGCCGGCTGACCGGGCCCAAGCACTCTGACTGCCCTGGCCCTGCCATTCACACCAC 954
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
DB 955 AGTGGCATCTGTGAGCTGCACTGCCAGCCCTGCTCACCTACCAACACAGACAGCTTTGAG 1014
QY 281 SerMetProAsnProGluGlyArgTyrrThrPheGlyAlaSerCysValThrAlaCysPro 300
DB 1015 TCCATGCCCAATCCCGAGGGCGGTATACATTCGGGCCAGCTGTGTGACTGCTGTGCC 1074
QY 301 TyrAsnTyrrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
DB 1075 TACAACCTACCTTTCTACGGAGTGGGATCTCGACCCCTGCTGCCCCCTGCAACACCAA 1134
QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
DB 1135 GAGGTGACAGCAGGATGGAACACAGCGGTGTGAGAGTGCAGAGCCCTGTGTGCCGA 1194
QY 341 ValCysTyrrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360

DB 1195 GTGTGCTATGCTCTGGCATGGAGCACTTGGAGAGGTGAGGGCAGTTACCAGTCCCAAT 1254
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DB 1255 ATCCAGAGTTTGTGCTGGCTGCAAGAGATCTTTGGAGCCCTGGCATTTCTGCGGAGAGC 1314
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
DB 1315 TTTGATGGGAGCCAGCTCCAACTGCCCCCTCCAGCCAGAGCAGCTCAAGTGTGT 1374
QY 401 GluThrLeuGluGluIleThrGlyTyrrLeuTyrrIleSerAlaTrpProAspSerLeuPro 420
DB 1375 GAGACTCTGGAAGAGATCACAGGTACTATATCTTCAGCATYGCCGACAGCTGTCT 1434
QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
DB 1435 GACTCAGCTCTTCCAGAACCTGCAAGTAATCCGGGAGCAATCTGCAATGGCGCC 1494
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
DB 1495 TACTGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGCGCTCACTGAGGGA 1554
QY 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
DB 1555 CTGGGAGTGGACTGGCCCTCATCCACCATTAACACCCACTCTCTCTGTCACACGGTG 1614
QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
DB 1615 CCCTGGGACCACTCTTTCCGNAACCCGACCAAGCTCTGCTCCACACTGCCAACCGGCA 1674
QY 501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
DB 1675 GAGGACGAGTGTGTGGCGAGGGCTGGCCCTGCCACCACTGTCGCCCGAGGCACTGC 1734
QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
DB 1735 TGGGTCACAGGGCCCACTGAGTGTCACTGACGAGCAGTTCTCTGGGGCCAGAGTGC 1794
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrrValAsnAlaArgHisCys 560
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DB 1915 GCTGACAGTGTGTGGCTGTGGCCCACTATAAGGACCCCTCCCTCTGCGTGGCCCGCTGC 1974
QY 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
DB 1975 CCAGCGGTGTGAACCTGACCTCTCTCATATGCCCACTGGAAGTTTCCAGATGAGGAG 2034
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
DB 2035 GGGGCAATGCCAGCTTGGCCCACTCACTGACCACTCTCTGTGTGGAGCTGATGATGACAAG 2094
QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
DB 2095 GGCTGCCCCCGAGCAGAGCGCCCTCTGACGTCCATCATCTCTGCGGTGGTGGC 2154
QY 653 ----- 653
DB 2155 ATTCTGCTGTGCTGTGCTTGGGGGTGCTCTTTGGGATCTCTCATCAAGCGACGAGCAG 2214
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DB 2215 AAGATCCGGAAGTACAGATGCGGAGACTGCTGCGGAAACGGAGCTGTGTGGAGCCGCTG 2274
QY 653 ----- 653
DB 2275 ACACCTAGCGGAGCGATGCCCAACCGAGCGCAGATCGGATCTCTGAAGAAGACGAGCTG 2334

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Db	955	AGT	GGC	AT	CT	GT	GAG	CT	GC	A	CT	GC	CC	CC	GG	T	AT	CA	CT	GC	CA	CA	1014	
Qy	281	Ser	Met	Pro	Asn	Pro	Glu	Gly	Arg	Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro		300	
Db	1015	TCC	AT	GCC	CA	AT	CCC	AGG	CCG	GT	AT	CA	TT	T	GGC	CC	AG	CT	GT	GT	GA	CT	1074	
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Qy	341	Val	Cys	Tyr	Gly	Leu	Gly	Met	Glu	His	Leu	Arg	Glu	Val	Arg	Ala	Val	Thr	Ser	Ala	Asn		360	
Db	1195	GTG	TG	CT	AT	TG	CT	T	GGG	CA	TGG	AG	CA	CT	T	GG	AG	GT	GAG	GG	CA	GT	AC	1254
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Qy	381	Phe	Asp	Gly	Asp	Pro	Ala	Ser	Asn	Thr	Ala	Pro	Leu	Gln	Pro	Glu	Gln	Leu	Gln	Val	Phe		400	
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Db	1555	CTG	GG	CAG	TG	AG	CT	TGG	CC	CT	AT	CC	AC	AT	AA	CAC	CC	CA	CT	CT	GT	CT	GC	1614
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Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3175 GACAGCACCCTTCTACCGCTCACTGTGTGGAGACGATGACATGGGGGACCTGTGTGGATGCT 3234
Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyValaGly 704
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Qy 705 GlyMetValHisHisArgHisArg 712
Db 3295 GGCATGTGTCCACCCAGGACCGC 3318
RESULT 13
US-10-101-510-81
; Sequence 81, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; PRIORITY FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-81
Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservatives: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 15 Gaps: 1
US-09-493-480-7 (1-712) x US-10-101-510-81 (1-4473)
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Db 175 ATGGAGCTGGCGGCTTGTGGCGCTGGGGGCTCTCTCTCGCCCTCTTGGCCCGCGAGCC 234
Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLeuLeuLeuProAlaSerProGlu 40
Db 235 GCGAGCACCAGTGTGACCGCGCACAGATGAAGCTGGCGCTCTCTCGCGAGTCCCGAG 294
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 295 ACCACCTGGACATGCTCGCCACCTCTACCGGGCTGCGAGGTGGTGGCAGGAAACCTG 354
Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 355 GAACTCACCTACTGCGCCACCAATGCGAGCTGTCTCTCGCGAGTATATCCAGGAGGTG 414
Qy 81 GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
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Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
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RESULT 15

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; Publication No. US2003022493A1
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; APPLICANT: Land, Hartmut
; APPLICANT: Deleu, Laurent
; TITLE OF INVENTION: COMPOSITIONS THAT INHIBIT PROLIFERATION
; TITLE OF INVENTION: OF CANCER CELLS
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; FILE REFERENCE: 21108.0005U3
; CURRENT APPLICATION NUMBER: US/10/392,113
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: 60/365,078
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: PCT/US01/32127
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/239,705
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence./Note =
; OTHER INFORMATION: Synthetic Construct
US-10-392-113-45
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Alignment Scores:

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Percent Similarity:	67.94%	Conservative:	0
Best Local Similarity:	67.94%	Mismatches:	0
Query Match:	95.50%	Indels:	336
DB:	13	Gaps:	1

US-09-493-480-7 (1-712) x US-10-392-113-45 (1-4530)

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268.525 Million cell updates/sec

Title: SEQ3-SEQ4

Perfect score: 158

Sequence: 1 DKGCPAQRASPLTSYRSLLDDDDGDLVD 30

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-Q-gapop 10.0 , Ygapext 0.5	
Ygapop 6.0 , Rgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	89	56.3	3768	2	US-08-356-786-1
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4	89	56.3	4473	2	US-09-048-804-1
5	89	56.3	4473	3	US-09-056-105-26
6	89	56.3	4473	4	US-09-663-834A-3
7	89	56.3	4530	1	US-08-229-515A-9
8	89	56.3	4530	1	US-08-645-865-9
9	89	56.3	4530	4	US-09-167-322-4
10	89	56.3	4530	4	US-09-527-487-1
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15	80	50.6	153	3	US-08-776-251-3	Sequence 3, Appl
16	80	50.6	201	4	US-09-200-355-3	Sequence 3, Appl
17	80	50.6	816	3	US-08-776-251-10	Sequence 10, Appl
18	80	50.6	2385	2	US-09-146-283-3	Sequence 3, Appl
19	80	50.6	2385	2	US-08-579-823A-3	Sequence 3, Appl
20	80	50.6	2385	3	US-09-344-195-3	Sequence 3, Appl
21	57	36.1	410	3	US-08-604-931-11	Sequence 11, Appl
22	57	36.1	410	3	US-09-363-639-11	Sequence 11, Appl
23	57	36.1	576	1	US-08-783-275-3	Sequence 3, Appl
24	57	36.1	576	1	US-08-727-708-3	Sequence 3, Appl
25	57	36.1	576	2	US-08-766-677-1	Sequence 1, Appl
26	57	36.1	576	2	US-08-843-951-1	Sequence 1, Appl
c 27	56	35.4	1830121	4	US-09-557-884-1	Sequence 1, Appl
c 28	56	35.4	1830121	4	US-09-643-990A-1	Sequence 1, Appl
29	54	34.2	5532	2	US-08-475-035-3	Sequence 3, Appl
30	54	34.2	5532	4	US-09-676-610B-17	Sequence 17, Appl
31	54	34.2	197496	4	US-09-877-177A-10	Sequence 10, Appl
32	53	33.5	2754	2	US-09-028-361A-1	Sequence 1, Appl
33	53	32.9	13321	4	US-08-956-171E-4	Sequence 4, Appl
c 34	51	32.3	5509	4	US-09-865-621A-1	Sequence 1, Appl
c 35	50	31.6	4403765	3	US-09-103-840A-2	Sequence 2, Appl
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39	49	31.0	2506	4	US-03-277-457-1	Sequence 1, Appl
40	49	31.0	2506	4	US-09-679-729-1	Sequence 1, Appl
41	49	31.0	3306	4	US-09-770-170-7	Sequence 7, Appl
42	49	31.0	10825	3	US-08-652-265-1	Sequence 1, Appl
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44	49	31.0	10825	3	US-08-652-265-5	Sequence 5, Appl
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47	49	31.0	10825	3	US-08-834-497A-3	Sequence 3, Appl
48	49	31.0	10825	3	US-08-834-497A-5	Sequence 5, Appl
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53	49	31.0	10825	3	US-09-503-444A-7	Sequence 7, Appl
54	49	31.0	12146	4	US-09-277-457-27	Sequence 27, Appl
55	49	31.0	12146	4	US-09-679-729-27	Sequence 27, Appl
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58	49	31.0	246240	2	US-08-724-394A-20	Sequence 20, Appl
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61	48.5	30.7	267	4	US-09-313-294A-1859	Sequence 1859, Ap
62	48.5	30.7	467	4	US-09-621-976-2248	Sequence 2248, Ap
63	48.5	30.7	3787	4	US-08-956-171E-375	Sequence 375, App
c 64	48	30.4	1284	4	US-09-894-844-106	Sequence 106, App
c 65	48	30.4	4422	4	US-09-166-350-1	Sequence 1, Appl
66	48	30.4	7970	1	US-08-135-511-31	Sequence 31, Appl
67	48	30.4	7970	1	US-08-187-453-31	Sequence 31, Appl
68	48	30.4	7970	1	US-08-562-985A-7	Sequence 7, Appl
69	48	30.4	24979	2	US-08-147-777-3	Sequence 3, Appl
70	48	30.4	24979	3	US-08-452-872-3	Sequence 3, Appl
71	48	30.4	24979	5	PCT-US93-03985-3	Sequence 3, Appl
c 72	48	30.4	35100	2	US-08-770-379-17	Sequence 17, Appl
c 73	48	30.4	35100	3	US-08-757-669A-17	Sequence 17, Appl
c 74	48	30.4	35100	4	US-09-230-371A-17	Sequence 17, Appl
75	47.5	30.1	564	4	US-09-134-001C-2343	Sequence 2343, Ap
76	47.5	30.1	1913	4	US-09-016-434-1314	Sequence 1314, Ap
77	47.5	30.1	2467	4	US-09-872-733A-3	Sequence 3, Appl
78	47.5	30.1	4338	4	US-09-872-733A-1	Sequence 1, Appl
79	47.5	30.1	8366	4	US-09-872-733A-6	Sequence 6, Appl
80	47.5	30.1	11561	2	US-08-450-332-1	Sequence 1, Appl
81	47.5	30.1	11561	2	US-08-637-640-1	Sequence 1, Appl
82	47.5	30.1	11561	3	US-09-004-406C-1	Sequence 1, Appl
83	47.5	30.1	33000	3	US-09-215-694-18	Sequence 18, Appl
84	47.5	29.7	305	3	US-09-299-843A-21	Sequence 21, Appl
85	47	29.7	305	4	US-09-088-337B-21	Sequence 21, Appl

c 86 47 29.7 558 4 US-09-280-116-185 Sequence 185, App
87 47 29.7 564 4 US-09-489-039A-6153 Sequence 6153, Ap
88 47 29.7 564 4 US-09-621-976-15297 Sequence 15297, A
89 47 29.7 1563 4 US-09-252-991A-12880 Sequence 12880, A
90 47 29.7 1623 4 US-09-252-991A-12572 Sequence 12572, A
91 47 29.7 1638 4 US-09-252-991A-16400 Sequence 16400, A
92 47 29.7 1917 4 US-09-499-203-15 Sequence 15, Appl
93 47 29.7 2229 4 US-09-252-991A-16088 Sequence 16088, A
94 47 29.7 2532 4 US-09-252-991A-12912 Sequence 12912, A
95 47 29.7 3489 4 US-09-252-991A-16193 Sequence 16193, A
96 47 29.7 3970 4 US-09-499-203-14 Sequence 14, Appl
97 47 29.7 4066 4 US-09-499-203-16 Sequence 16, Appl
98 47 29.7 6204 4 US-09-499-203-20 Sequence 20, Appl
99 47 29.7 7387 4 US-09-499-203-17 Sequence 17, Appl
100 47 29.7 9321 4 US-09-499-203-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-625-101-1
; Sequence 1, Application US/08625101
; Patent No. 5869445
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
; TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
; TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
; TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/625,101
; FILING DATE: 01-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3768 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3765
US-08-625-101-1

Alignment Scores: Length: 3768
Pred. No.: 6.95e-05 Matches: 20
Score: 89.00 Conservative: 0
Percent Similarity: 86.96% Mismatches: 1
Best Local Similarity: 86.96% Indels: 2
Query Match: 56.33% Gaps: 1
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Db 3049 CTGGTGGAT 3057
RESULT 2
US-08-356-786-1
; Sequence 1, Application US/08356786
; Patent No. 5877305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; TITLE OF INVENTION: Marker
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESS: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,786
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/831,967
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3768 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3768
; OTHER INFORMATION: /note= "product = "cerB-b2"
US-08-356-786-1

Alignment Scores: Length: 3768
Pred. No.: 6.95e-05 Matches: 20
Score: 89.00 Conservative: 0
Percent Similarity: 86.96% Mismatches: 1
Best Local Similarity: 86.96% Indels: 2
Query Match: 56.33% Gaps: 1
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Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuAlaAspAspMetGlyAsp 27
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Db 2989 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3048
Qy 28 LeuValasp 30
Db 3049 CTGGTGGAT 3057

RESULT 3
US-09-811-115-2
; Sequence 2, Application US/09811115
; Patent No. 6632979
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT.034A
; CURRENT APPLICATION NUMBER: US/09/811,115
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-115-2

Alignment Scores:
Pred. No.: 6,95e-05 Length: 3768
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
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SEQ3-SEQ4 (1-30) x US-09-811-115-2 (1-3768)
Qy 10 AlaserProLeu-----ThrsTyrArgSerLeuLeuGluAspAspMetGlyasp 27
Db 2989 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3048
Qy 28 LeuValasp 30
Db 3049 CTGGTGGAT 3057

RESULT 4
US-09-048-804-1
; Sequence 1, Application US/09048804
; Patent No. 5968748
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett, Allan Lipton, Lois M. Witters
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF
; TITLE OF INVENTION: HUMAN HER-2 EXPRESSION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 5968748ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/048,804
; FILING DATE: Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
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; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-2913
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4473 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Unknown
; ANTI-SENSE: NO
US-09-048-804-1

Alignment Scores:
Pred. No.: 8,75e-05 Length: 4473
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 2 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-048-804-1 (1-4473)
Qy 10 AlaserProLeu-----ThrsTyrArgSerLeuLeuGluAspAspMetGlyasp 27
Db 3163 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3222
Qy 28 LeuValasp 30
Db 3223 CTGGTGGAT 3231

RESULT 5
US-09-056-105-26
; Sequence 26, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
; APPLICANT: KIPPS, THOMAS J.
; APPLICANT: WU, YUNQI
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
; TITLE OF INVENTION: PROCESSING
; FILE REFERENCE: 233/221
; CURRENT APPLICATION NUMBER: US/09/056,105
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: 60/043,467
; EARLIER FILING DATE: 1997-04-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-056-105-26

Alignment Scores:
Pred. No.: 8,75e-05 Length: 4473
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 3 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-056-105-26 (1-4473)
Qy 10 AlaserProLeu-----ThrsTyrArgSerLeuLeuGluAspAspMetGlyasp 27
Db 3163 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3222
Qy 28 LeuValasp 30
Db 3223 CTGGTGGAT 3231

RESULT 6
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US-09-663-834A-3
; Sequence 3, Application US/09663834A
; Patent No. 6613567

GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowbert
; TITLE OF INVENTION: ANTISENSE MODULATION OF HER-2 EXPRESSION
; FILE REFERENCE: RTS-0033
; CURRENT APPLICATION NUMBER: US/09/663,834A
; CURRENT FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 3
; LENGTH: 4473
; TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (175)...(3942)

US-09-663-834A-3
Alignment Scores:
Pred. No.: 8,75e-05 Length: 4473
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservatives: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 4 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-663-834A-3 (1-4473)
Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 3163 GCACGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3222
Qy 28 LeuValasp 30
Db 3223 CTGGTGGAT 3231

RESULT 7

US-08-229-515A-9
; Sequence 9, Application US/08229515A
; Patent No. 5518885

GENERAL INFORMATION:
; APPLICANT: RAZI UDDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,515A
FILING DATE: 19 APR 1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.608
TELEPHONE: 404-688-0770
TELEFAX: 404-688-9880
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4530 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-645-865-9
Alignment Scores:
Pred. No.: 8,9e-05 Length: 4530
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservatives: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 1 Gaps: 1

SEQ3-SEQ4 (1-30) x US-08-229-515A-9 (1-4530)
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Db 3139 GCACGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3198
Qy 28 LeuValasp 30
Db 3199 CTGGTGGAT 3207

RESULT 8

US-08-645-865-9
; Sequence 9, Application US/08645865
; Patent No. 5654406

GENERAL INFORMATION:
; APPLICANT: RAZI UDDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,865
FILING DATE: 14 MAY 1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.608
TELEPHONE: 404-688-0770
TELEFAX: 404-688-9880
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4530 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-645-865-9
Alignment Scores:
Pred. No.: 8,9e-05 Length: 4530
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservatives: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 1 Gaps: 1

SEQ3-SEQ4 (1-30) x US-08-645-865-9 (1-4530)

Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 3139 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGATGGGGGAC 3198
Qy 28 LeuValAsp 30
Db 3199 CTGGTGGAT 3207

RESULT 9

US-09-167-322-4
; Sequence 4, Application US/09167322
; Patent No. 6365151
; GENERAL INFORMATION:
; APPLICANT: Allegheny University of the Health
; Sciences, Halpern, Michael S.
; England, James M.
; TITLE OF INVENTION: CANCER VACCINE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorigna & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/167,322
; FILING DATE: 07-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/00582
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 7933-33 PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; INFORMATION FOR SEQ ID NO: 4:
; LENGTH: 4530 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-167-322-4

Alignment Scores:
Pred. No.: 8.9e-05 Length: 4530
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 4 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-167-322-4 (1-4530)

Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 3139 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGATGGGGGAC 3198
Qy 28 LeuValAsp 30
Db 3199 CTGGTGGAT 3207

RESULT 10

US-09-527-487-1
; Sequence 1, Application US/09527487
; Patent No. 6528060
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: HER2 ANTIGENIC PEPTIDES
; FILE REFERENCE: 126881309200
; CURRENT APPLICATION NUMBER: US/09/527,487
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1

LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (151)..(3915)
US-09-527-487-1

Alignment Scores:
Pred. No.: 8.9e-05 Length: 4530
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 4 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-527-487-1 (1-4530)

Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 3139 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGATGGGGGAC 3198

Qy 28 LeuValAsp 30
Db 3199 CTGGTGGAT 3207

RESULT 11

US-09-877-177A-11
; Sequence 11, Application US/09877177A
; Patent No. 6582919
; GENERAL INFORMATION:
; APPLICANT: K. Danenberg
; TITLE OF INVENTION: Method of determining Epidermal Growth
; TITLE OF INVENTION: Factor Receptor and HER2-Neu Gene Expression
; TITLE OF INVENTION: and Correlation of Levels Thereof With Survival
; FILE REFERENCE: 11220/120
; CURRENT APPLICATION NUMBER: US/09/877,177A
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11

LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-877-177A-11

Alignment Scores:
Pred. No.: 8.9e-05 Length: 4530
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 4 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-877-177A-11 (1-4530)

Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 3139 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGATGGGGGAC 3198

```
Qy      28 LeuValasp 30
Db      3199 CTGGTGGAT 3207

RESULT 12
US-09-811-115-1
; Sequence 1, Application US/09811115
; Patent No. 6632979
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT 034A
; CURRENT APPLICATION NUMBER: US/09/811,115
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9274
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Vector Sequence
US-09-811-115-1

Alignment Scores:
Pred. No.:      0.000233      Length:      9274
Score:          89.00      Matches:      20
Percent Similarity: 86.96%      Conservative: 0
Best Local Similarity: 86.96%      Mismatches: 1
Query Match:      56.33%      Indels:      2
DB:              4      Gaps:      1

SEQ3-SEQ4 (1-30) x US-09-811-115-1 (1-9274)
Qy      10 AlaSerProLeu-----ThrSerTyArgSerLeuLeuGluAspAspMetGlyAsp 27
Db      4719 GCAGTCCCTTGACAGCAGCCTTCTACCGCTCACTCTGAGGAGCAGATGATGATGGGGGAC 4778

Qy      28 LeuValasp 30
Db      4779 CTGGTGGAT 4787

RESULT 13
US-08-229-515A-14
; Sequence 14, Application US/08229515A
; Patent No. 5518885
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 19 APR 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELEPHONE: 404-688-9880
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3955 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-645-865-14

Qy      10 AlaSerProLeu-----ThrSerTyArgSerLeuLeuGluAspAspMetGlyAsp 27
Db      3020 TCCAGCCCCATGGACAGTACTTCTACCGCTTCACTCTGAGGAGATGATGATGGGGTGC 3079

Qy      28 LeuValasp 30
Db      3080 CTGGTAGAC 3088

RESULT 14
US-08-645-865-14
; Sequence 14, Application US/08645865
; Patent No. 5654406
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 14 MAY 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELEPHONE: 404-688-9880
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3955 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-645-865-14

NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.608
TELEPHONE: 404-688-9880
TELEFAX: 404-688-9880
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3955 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-645-865-14
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Qy 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
|||
Db 10 GACAAGGGCTGCCCGCCGAGCAGAGCCAGCCCTCTGACGTCC 54

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RESULT 17
US-08-776-251-10
; Sequence 10, Application US/08776251
; Patent No. 6025340
; GENERAL INFORMATION:
; APPLICANT: Springer, Caroline J
; APPLICANT: Marais, Richard
; TITLE OF INVENTION: Surface expression of enzyme i
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye
; STREET: 1100 No. 6025340th Glebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,251
; FILING DATE: 31-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01782
; FILING DATE: 27-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9415167.7
; FILING DATE: 27-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Arthur R. Crawford
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 620-20
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 816 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

```



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Alignment Scores:
Pred. No.:      0.00124      Length:      2385
Score:          80.00       Matches:      15
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:      50.63%     Indels:      0
DB:              3          Gaps:       0

SEQ3-SEQ4 (1-30) x US-09-344-195-3 (1-2385)

Qy      1 AspiysgClvCsProAlaGluGlnArgAlaSerProLeuThrSer 15
Db      1925 GACAAGGGCTGCCCGCGCGAGCAGAGCCGCTCTGACGTC 1969

RESULT 21
US-08-604-991-11
; Sequence 11, Application US/08604991
; Patent No. 6001565
; GENERAL INFORMATION:
; APPLICANT: Fox, Andrew J.
; APPLICANT: Jones, Dennis Mackay
; TITLE OP INVENTION: Detection and Speciation of
; TITLE OF INVENTION: Campylobacter
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA

```

```

225 AGCCCTACAGATTCGAAGTTTATCGCACCTGATGGAGGAGGACATCGGAGACATT 284
29 Valasp 30
285 GTGGAT 290

RESULT 22
US-09-363-639-11
: Sequence 11, Application US/09363639
: Patent No. 6080547
: GENERAL INFORMATION:
: APPLICANT: Fox, Andrew J.
: APPLICANT: Jones, Dennis Mackay
: TITLE OF INVENTION: Detection and Speciation of
: TITLE OF INVENTION: Campylobacter
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
: STREET: 1100 New York Avenue, NW, Suite 600
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/09/363,639
FILING DATE: 30-JUL-1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/604,991
FILING DATE: 29-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB94/01967
FILING DATE: 09-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9318751.6
FILING DATE: 09-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Remond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0040001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-317-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-363-639-11

Alignment Scores:
Pred. No.: 0.893 Length: 410
Score: 57.00 Matches: 12
Percent Similarity: 77.27% Conservative: 5
Best Local Similarity: 54.55% Mismatches: 3
Query Match: 36.08% Indels: 2
DB: 1
Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-363-639-11 (1-410)

QY 11 SerProLeuThrSer-----TyrArgSerLeuLeuGluAspAspMetGlyAspLeu 28
|||||
Db 225 AGCCCTACAGATTCACAGTTTATCGCACCTGATCGAGGAGGACATGGACACATT 284
QY 29 ValAsp 30
|||||
Db 285 GTGGAT 290

RESULT 23
US-08-783-275-3
Sequence 3, Application US/08783275
Patent No. 5766859
GENERAL INFORMATION:
APPLICANT: Vojdani, Aristo
APPLICANT: Mordechai, Eli
TITLE OF INVENTION: RIBONUCLEASE L INHIBITOR AS
TITLE OF INVENTION: AN INDICATOR OF CHRONIC FATIGUE SYNDROME
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,275
FILING DATE: 15-JAN-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/727,708
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bartfeld, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: IMSCI.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-783-275-3

Alignment Scores:
Pred. No.: 1.41 Length: 576
Score: 57.00 Matches: 12
Percent Similarity: 77.27% Conservative: 5
Best Local Similarity: 54.55% Mismatches: 3
Query Match: 36.08% Indels: 2
DB: 1
Gaps: 1

SEQ3-SEQ4 (1-30) x US-08-783-275-3 (1-576)

QY 11 SerProLeuThrSer-----TyrArgSerLeuLeuGluAspAspMetGlyAspLeu 28
|||||
Db 222 AGCCCTACAGATTCACAGTTTATCGCACCTGATCGAGGAGGACATGGACACATT 281
QY 29 ValAsp 30
|||||
Db 282 GTGGAT 287

RESULT 24
US-08-727-708-3
Sequence 3, Application US/08727708
Patent No. 5776690
GENERAL INFORMATION:
APPLICANT: Vojdani, Aristo
APPLICANT: Mordechai, Eli
TITLE OF INVENTION: RIBONUCLEASE L INHIBITOR AS
TITLE OF INVENTION: AN INDICATOR OF CHRONIC FATIGUE SYNDROM
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/727,708
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bartfeld, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: IMSCI.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550

```

; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 576 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-727-708-3

Alignment Scores:
Pred. No.: 1.41 Length: 576
Score: 57.00 Matches: 12
Percent Similarity: 77.27% Conservative: 5
Best Local Similarity: 54.55% Mismatches: 3
Query Match: 36.08% Indels: 2
DB: Gaps: 1

SEQ3-SEQ4 (1-30) x US-08-727-708-3 (1-576)
Qy 11 SerProLeuThrSer-----TyrArgSerLeuLeuGluAspAspMetGlyAspLeu 28
Db 222 AGCCCTACAGATTCCAAGTTTATCGCACCTGATGGAGGAGGAGGACATGGAGACATT 281
Qy 29 Valasp 30
Db 282 GTGGAT 287

RESULT 25
US-08-766-677-1
; Sequence 1, Application US/08766677
; Patent No. 5830668
; GENERAL INFORMATION:
; APPLICANT: Vojdani, Aristo
; APPLICANT: Mordechai, Eli
; TITLE OF INVENTION: Detection of Chronic Fatigue
; TITLE OF INVENTION: Syndrome
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive Sixteenth Flo
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,677
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/766,677
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: IMSCI.002A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714/760-0404
; TELEFAX: 714/760-9503
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 576 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-766-677-1

Alignment Scores:
Pred. No.: 1.41 Length: 576
Score: 57.00 Matches: 12
Percent Similarity: 77.27% Conservative: 5
Best Local Similarity: 54.55% Mismatches: 3
Query Match: 36.08% Indels: 2
DB: Gaps: 1

SEQ3-SEQ4 (1-30) x US-08-727-708-3 (1-576)
Qy 11 SerProLeuThrSer-----TyrArgSerLeuLeuGluAspAspMetGlyAspLeu 28
Db 222 AGCCCTACAGATTCCAAGTTTATCGCACCTGATGGAGGAGGAGGACATGGAGACATT 281
Qy 29 Valasp 30
Db 282 GTGGAT 287

RESULT 26
US-08-843-951-1
; Sequence 1, Application US/08843951
; Patent No. 5853996
; GENERAL INFORMATION:
; APPLICANT: Vojdani, Aristo
; APPLICANT: Mordechai, Eli
; TITLE OF INVENTION: Detection of Chronic Fatigue
; TITLE OF INVENTION: Syndrome
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive Sixteenth Flo
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/843,951
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/766,677
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: IMSCI.002A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714/760-0404
; TELEFAX: 714/760-9503
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 576 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-843-951-1

Alignment Scores:
Pred. No.: 1.41 Length: 576
Score: 57.00 Matches: 12
Percent Similarity: 77.27% Conservative: 5
Best Local Similarity: 54.55% Mismatches: 3
Query Match: 36.08% Indels: 2
DB: Gaps: 1

SEQ3-SEQ4 (1-30) x US-08-766-677-1 (1-576)
Qy 11 SerProLeuThrSer-----TyrArgSerLeuLeuGluAspAspMetGlyAspLeu 28
Db 222 AGCCCTACAGATTCCAAGTTTATCGCACCTGATGGAGGAGGAGGACATGGAGACATT 281
Qy 29 Valasp 30
Db 282 GTGGAT 287

RESULT 26
US-08-843-951-1
; Sequence 1, Application US/08843951
; Patent No. 5853996
; GENERAL INFORMATION:
; APPLICANT: Vojdani, Aristo
; APPLICANT: Mordechai, Eli
; TITLE OF INVENTION: Detection of Chronic Fatigue
; TITLE OF INVENTION: Syndrome
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive Sixteenth Flo
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/843,951
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/766,677
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: IMSCI.002A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714/760-0404
; TELEFAX: 714/760-9503
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 576 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-843-951-1

Alignment Scores:
Pred. No.: 1.41 Length: 576
Score: 57.00 Matches: 12
Percent Similarity: 77.27% Conservative: 5
Best Local Similarity: 54.55% Mismatches: 3
Query Match: 36.08% Indels: 2
DB: Gaps: 1
```


GENERAL INFORMATION:
; APPLICANT: KING, C. R.
; APPLICANT: KRAUS, MATTHIAS H.
; APPLICANT: AARONSON, STUART A.
; TITLE OF INVENTION: HUMAN GENE RELATED TO BUT DISTINCT FROM
; TITLE OF INVENTION: EGF RECEPTOR GENE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/475.035
; APPLICATION NUMBER: US/08/475.035
; FILING DATE: 7 Jun 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perryman, David G.
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.656
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5532 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 187..3816
; US-08-475-035-3

Alignment Scores:
Pred. No.: 94.7 Length: 5532
Score: 54.00 Matches: 11
Percent Similarity: 77.27% Conservative: 6
Best Local Similarity: 50.00% Mismatches: 3
Query Match: 34.18% Indels: 2
DB: 2 Gaps: 1

SEQ3-SEQ4 (1-30) x US-08-475-035-3 (1-5532)

Qy 11 SerProLeuThrSer-----TyrArgSerLeuLeuGluAspAspMetGlyAspLeu 28
Db 3157 AGTCCTACAGACTCCAACTTCTACCGTGCCTGTGATGAAGAGACATGGACGCGTG 3216
Qy 29 ValAsp 30
Db 3217 GTGGAT 3222

RESULT 30

US-09-676-610B-17
; Sequence 17, Application US/09676610B
; Patent No. 644465
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
; FILE REFERENCE: RTS-0138
; CURRENT APPLICATION NUMBER: US/09/676.610B
; CURRENT FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 182

; SEQ ID NO 17
; LENGTH: 5532
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (187)...(3819)
US-09-676-610B-17
Alignment Scores:
Pred. No.: 94.7 Length: 5532
Score: 54.00 Matches: 11
Percent Similarity: 77.27% Conservative: 6
Best Local Similarity: 50.00% Mismatches: 3
Query Match: 34.18% Indels: 2
DB: 4 Gaps: 1
SEQ3-SEQ4 (1-30) x US-09-676-610B-17 (1-5532)
Qy 11 SerProLeuThrSer-----TyrArgSerLeuLeuGluAspAspMetGlyAspLeu 28
Db 3157 AGTCCTACAGACTCCAACTTCTACCGTGCCTGTGATGAAGAGACATGGACGCGTG 3216
Qy 29 ValAsp 30
Db 3217 GTGGAT 3222
Search completed: June 8, 2004, 08:59:40
Job time : 742 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 8, 2004, 06:43:09 ; Search time 267 Seconds
(without alignments)
512.584 Million cell updates/sec

Title: SEQ3-SEQ4

Perfect score: 158

Sequence: 1 DKGCPAQRASPLTYSRLLEDMDGLVD 30

Scoring table:

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Ygapop 10.0	Ygapext 0.5	
Fgapop 6.0	Fgapext 7.0	
Delop 6.0	Delext 7.0	

Searched: 2995936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters: 5991872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Command line parameters:

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-DB=Published Applications NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=100 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=30 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=HOLLERAN480 @CNG 1.1 879 @runat_07062004_152436_24797
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=10 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:	1:	/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
	2:	/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
	3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
	4:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
	5:	/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
	6:	/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
	7:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
	8:	/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
	9:	/cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
	10:	/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
	11:	/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
	12:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
	13:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:
	14:	/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
	15:	/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq2:
	16:	/cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
	17:	/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
	18:	/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq2:
	19:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	89	56.3	1115	13	US-09-925-298-165	Sequence 165, App
2	89	56.3	1115	15	US-10-102-806-165	Sequence 165, App
3	89	56.3	1713	15	US-10-378-393-14	Sequence 14, Appl
4	89	56.3	1755	9	US-09-930-125-6	Sequence 6, Appl
5	89	56.3	1767	9	US-09-930-125-4	Sequence 4, Appl
6	89	56.3	1773	9	US-09-930-125-7	Sequence 7, Appl
7	89	56.3	1806	9	US-09-930-125-5	Sequence 5, Appl
8	89	56.3	2411	15	US-10-378-393-10	Sequence 10, Appl
9	89	56.3	3765	15	US-10-207-498-5	Sequence 5, Appl
10	89	56.3	3768	9	US-09-811-123-8	Sequence 8, Appl
11	89	56.3	3768	9	US-09-811-115-2	Sequence 2, Appl
12	89	56.3	3768	9	US-09-854-356-9	Sequence 9, Appl
13	89	56.3	3768	9	US-09-930-125-3	Sequence 1, Appl
14	89	56.3	3768	13	US-09-984-092-3	Sequence 3, Appl
15	89	56.3	3768	13	US-10-280-576-3	Sequence 3, Appl
16	89	56.3	3768	13	US-09-765-973-1	Sequence 1, Appl
17	89	56.3	3768	15	US-10-313-644-1	Sequence 1, Appl
18	89	56.3	4473	10	US-09-441-411-5	Sequence 5, Appl
19	89	56.3	4473	15	US-10-146-473-32	Sequence 32, Appl
20	89	56.3	4473	15	US-10-207-655-44	Sequence 44, Appl
21	89	56.3	4473	15	US-10-101-510-81	Sequence 81, Appl
22	89	56.3	4530	9	US-09-877-177-11	Sequence 11, Appl
23	89	56.3	4530	13	US-10-392-113-45	Sequence 45, Appl
24	89	56.3	4530	13	US-10-426-836-11	Sequence 11, Appl
25	89	56.3	4530	15	US-10-177-293-125	Sequence 125, App
26	89	56.3	4530	15	US-10-007-926A-119	Sequence 119, App
27	89	56.3	4530	15	US-10-338-730-1	Sequence 1, Appl
28	89	56.3	4530	15	US-10-101-510-124	Sequence 124, App
29	89	56.3	4530	16	US-10-116-275-131	Sequence 131, App
30	89	56.3	4530	16	US-10-272-437A-27	Sequence 27, Appl
31	89	56.3	4530	16	US-10-117-937-595	Sequence 595, App
32	89	56.3	4530	16	US-10-159-563-208	Sequence 208, App
33	89	56.3	4530	16	US-10-435-696-10	Sequence 10, Appl
34	89	56.3	4543	10	US-09-769-508-1	Sequence 1, Appl
35	89	56.3	4543	10	US-09-971-392-70	Sequence 70, Appl
36	89	56.3	4642	15	US-10-198-846-10896	Sequence 10896, A
37	89	56.3	9274	9	US-09-811-123-7	Sequence 7, Appl
38	89	56.3	9274	9	US-09-811-115-1	Sequence 1, Appl
39	84	53.2	3955	9	US-09-870-759-117	Sequence 117, App
40	84	53.2	3955	9	US-09-854-356-10	Sequence 10, Appl
41	84	53.2	3955	10	US-09-751-708A-117	Sequence 117, App
42	80	50.6	201	14	US-10-109-213-3	Sequence 3, Appl
43	80	50.6	884	16	US-10-412-804A-7	Sequence 7, Appl
44	80	50.6	1479	16	US-10-412-804A-1	Sequence 1, Appl
45	80	50.6	2164	16	US-10-412-804A-5	Sequence 5, Appl
46	80	50.6	3771	9	US-09-854-356-11	Sequence 11, Appl
47	74	46.8	2149	16	US-10-412-804A-9	Sequence 9, Appl
48	63	39.9	2149	9	US-09-960-352-4186	Sequence 4186, Ap
49	57	36.1	1829	13	US-10-425-114-31106	Sequence 31106, A
50	56	35.4	1830121	15	US-10-329-960-1	Sequence 1, Appl
51	56	35.4	1830121	16	US-10-329-670-1	Sequence 1, Appl
52	55.5	35.1	441	9	US-09-864-761-3956	Sequence 3956, Ap
53	55.5	35.1	6236	13	US-10-381-327-16	Sequence 16, Appl
54	55	34.8	492	10	US-09-918-995-29035	Sequence 29035, A
55	54	34.2	376	13	US-10-027-632-55589	Sequence 55589, A
56	54	34.2	376	13	US-10-027-632-55589	Sequence 311744, A
57	54	34.2	376	16	US-10-027-632-55589	Sequence 55589, A
58	54	34.2	376	16	US-10-027-632-311744	Sequence 311744, A
59	54	34.2	520	9	US-09-867-701-7156	Sequence 7156, Ap
60	54	34.2	600	9	US-09-864-761-15913	Sequence 15913, A
61	54	34.2	3633	9	US-09-725-433-1	Sequence 1, Appl
62	54	34.2	3633	13	US-10-236-417-75	Sequence 75, Appl
63	54	34.2	5264	9	US-09-920-300A-1731	Sequence 1731, Ap
64	54	34.2	5264	14	US-10-033-528-1731	Sequence 1731, Ap
65	54	34.2	5264	15	US-10-099-926-1731	Sequence 73, Ap
66	54	34.2	5367	13	US-10-236-417-73	Sequence 73, Appl
67	54	34.2	5532	13	US-10-387-252-1	Sequence 1, Appl
68	54	34.2	5532	13	US-10-388-360-300	Sequence 300, App
69	54	34.2	5532	15	US-10-007-926A-137	Sequence 137, App
70	54	34.2	5532	15	US-10-101-510-95	Sequence 95, Appl
71	54	34.2	5532	16	US-10-380-931-17	Sequence 17, Appl
72	54	34.2	10058	9	US-09-974-298-98	Sequence 98, Appl

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-14

Alignment Scores:
Pred. No.: 4.59e-05 Length: 1713
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 15 Gaps: 1

SEQ3-SEQ4 (1-30) x US-10-378-393-14 (1-1713)

Qy 10 AlaSerProLeu-----ThrSerTyArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 934 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 993
Qy 28 LeuValAsp 30
Db 994 CTGGTGGAT 1002

RESULT 4

US-09-930-125-6

; Sequence 6, Application US/09930125
; Publication No. US20020193329A1

; GENERAL INFORMATION:

; APPLICANT: Hand-Zimmerman, Susan
; APPLICANT: Cheever, Martin A.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Vedvick, Thomas S.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.544

; CURRENT APPLICATION NUMBER: US/09/930.125

; CURRENT FILING DATE: 2001-08-14

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 6

; LENGTH: 1755

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-930-125-6

Alignment Scores:
Pred. No.: 4.73e-05 Length: 1755
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 9 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-930-125-6 (1-1755)

Qy 10 AlaSerProLeu-----ThrSerTyArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 967 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 1026
Qy 28 LeuValAsp 30
Db 1027 CTGGTGGAT 1035

RESULT 5

US-09-930-125-4

; Sequence 4, Application US/09930125
; Publication No. US20020193329A1

; GENERAL INFORMATION:

; APPLICANT: Hand-Zimmerman, Susan
; APPLICANT: Cheever, Martin A.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Vedvick, Thomas S.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.544

; CURRENT APPLICATION NUMBER: US/09/930.125

; CURRENT FILING DATE: 2001-08-14

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 4

; LENGTH: 1767

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-930-125-4

Alignment Scores:
Pred. No.: 4.77e-05 Length: 1767
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 9 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-930-125-4 (1-1767)

Qy 10 AlaSerProLeu-----ThrSerTyArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 967 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 1026
Qy 28 LeuValAsp 30
Db 1027 CTGGTGGAT 1035

RESULT 6

US-09-930-125-7

; Sequence 7, Application US/09930125

; Publication No. US20020193329A1

; GENERAL INFORMATION:

; APPLICANT: Hand-Zimmerman, Susan
; APPLICANT: Cheever, Martin A.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.544

; CURRENT APPLICATION NUMBER: US/09/930.125

; CURRENT FILING DATE: 2001-08-14

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 7

; LENGTH: 1773

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-930-125-7

Alignment Scores:
Pred. No.: 4.78e-05 Length: 1773
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 9 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-930-125-7 (1-1773)

QY 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 991 GCCAGTCCCTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 1050

QY 28 LeuValasp 30
Db 1051 CTGGTGGAT 1059

RESULT 7

US-09-930-125-5
; Sequence 5, Application US/09930125
; Publication No. US20020193329A1
; GENERAL INFORMATION:
; APPLICANT: Hand-Zimmerman, Susan
; APPLICANT: Cheever, Martin A.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia S.
; APPLICANT: Vedwick, Thomas S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.544
; CURRENT APPLICATION NUMBER: US/09/930,125
; CURRENT FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1806
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-930-125-5

Alignment Scores:
Pred. No.: 4.89e-05 Length: 1806
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 9 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-930-125-5 (1-1806)

QY 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 1024 GCCAGTCCCTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 1083

QY 28 LeuValasp 30
Db 1084 CTGGTGGAT 1092

RESULT 8

US-10-378-393-10
; Sequence 10, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 2411
; TYPE: DNA

; ORGANISM: Homo sapiens
US-10-378-393-10

Alignment Scores:
Pred. No.: 6.9e-05 Length: 2411
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 15 Gaps: 1

SEQ3-SEQ4 (1-30) x US-10-378-393-10 (1-2411)

QY 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 1632 GCCAGTCCCTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 1691

QY 28 LeuValasp 30
Db 1692 CTGGTGGAT 1700

RESULT 9

US-10-207-498-5
; Sequence 5, Application US/10207498
; Publication No. US20030143568A1
; GENERAL INFORMATION:
; APPLICANT: Elizabeth Singer
; APPLICANT: Ralf Landgraf
; APPLICANT: Dennis J. Slamon
; APPLICANT: David Eisenberg
; TITLE OF INVENTION: METHODS AND MATERIALS FOR CHARACTERIZING
; FILE REFERENCE: 30448.103-US-UI
; CURRENT APPLICATION NUMBER: US/10/207,498
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/308,431
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3765
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-10-207-498-5

Alignment Scores:
Pred. No.: 0.000117 Length: 3765
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 15 Gaps: 1

SEQ3-SEQ4 (1-30) x US-10-207-498-5 (1-3765)

QY 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 2989 GCCAGTCCCTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3048

QY 28 LeuValasp 30
Db 3049 CTGGTGGAT 3057

RESULT 10

US-09-811-123-8
; Sequence 8, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
; APPLICANT: Ralph Schwall

```
; APPLICANT: Mark Slikowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ETBB
; FILE REFERENCE: ANTIBODY-MAYTANSINOID CONJUGATES
; FILE REFERENCE: GENENT.073A2
; CURRENT APPLICATION NUMBER: US/09/811,123
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-123-8

Alignment Scores:
Pred. No.: 0.000117 Length: 3768
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 9 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-811-123-8 (1-3768)

Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 2989 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGATGGGGGAC 3048

Qy 28 LeuValAsp 30
Db 3049 CTGGTGGAT 3057

RESULT 11
US-09-811-115-2
; Sequence 2, Application US/09811115
; Patent No. US20020035736A1
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT.034A
; CURRENT APPLICATION NUMBER: US/09/811,115
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-115-2

Alignment Scores:
Pred. No.: 0.000117 Length: 3768
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 9 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-811-115-2 (1-3768)

Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 2989 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGATGGGGGAC 3048

Qy 28 LeuValAsp 30
```

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Db 3049 CTGGTGGAT 3057

RESULT 12
US-09-854-356-9
; Sequence 9, Application US/09854356
; Patent No. US20020177567A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Cheeysen, Dirk
; APPLICANT: Corixa Corporation
; APPLICANT: SmithKline Beecham Biologicals S. A.
; TITLE OF INVENTION: HER-2/neu Fusion Proteins
; FILE REFERENCE: 014058-009810PC
; CURRENT APPLICATION NUMBER: US/09/854,356
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 09/493,480
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,976
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3768)
; OTHER INFORMATION: human HER-2/neu protein
; NAME/KEY: misc_feature
; LOCATION: (1)..(1959)
; OTHER INFORMATION: extracellular domain (ECD) of human HER-2/neu
; NAME/KEY: misc_feature
; LOCATION: (2026)..(3765)
; OTHER INFORMATION: intracellular domain (ICD) of human HER-2/neu
; NAME/KEY: misc_feature
; LOCATION: (2968)..(3765)
; OTHER INFORMATION: phosphorylation domain (PD) of human HER-2/neu
; NAME/KEY: misc_feature
; LOCATION: (2968)..(3144)
; OTHER INFORMATION: preferred portion of the phosphorylation domain
; OTHER INFORMATION: (delta PD) of human HER-2/neu
US-09-854-356-9

Alignment Scores:
Pred. No.: 0.000117 Length: 3768
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 9 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-854-356-9 (1-3768)

Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 2989 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGATGGGGGAC 3048

Qy 28 LeuValAsp 30
Db 3049 CTGGTGGAT 3057

RESULT 13
US-09-930-125-1
; Sequence 1, Application US/09930125
; Publication No. US20020193329A1
; GENERAL INFORMATION:
; APPLICANT: Hand-Zimmerman, Susan
; APPLICANT: Cheever, Martin A.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Kalos, Michael D.
```

```
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Vedvick, Thomas S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES
; FILE REFERENCE: 210121.544
; CURRENT APPLICATION NUMBER: US/09/930,125
; CURRENT FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-09-930-125-1

Alignment Scores:
Pred. No.: 0.000117 Length: 3768
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 9 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-930-125-1 (1-3768)
Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuGluAspMetGlyAsp 27
Db 2989 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCTGCTGGAGGACGATGACATGGGGGAC 3048

Qy 28 LeuValAsp 30
Db 3049 CTGGTGGAT 3057

RESULT 14
US-09-984-092-3
; Sequence 3, Application US/09984092
; Publication No. US20040037840A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL THERAPEUTIC VACCINE FORMULATIONS
; FILE REFERENCE: P101PC00
; CURRENT APPLICATION NUMBER: US/09/984,092
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3768)
US-09-984-092-3

Alignment Scores:
Pred. No.: 0.000117 Length: 3768
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 13 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-984-092-3 (1-3768)
Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuGluAspMetGlyAsp 27
Db 2989 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCTGCTGGAGGACGATGACATGGGGGAC 3048

Qy 28 LeuValAsp 30
Db 3049 CTGGTGGAT 3057

RESULT 15
US-10-280-576-3
; Sequence 3, Application US/10280576
; Publication No. US20040044405A1
; GENERAL INFORMATION:
; APPLICANT: Wolffe, Matthew R.
; TITLE OF INVENTION: VASCULAR STENT OR GRAFT COATED OR IMPREGNATED WITH PROTEIN
; FILE REFERENCE: 09820.189
; CURRENT APPLICATION NUMBER: US/10/280,576
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 60/343,732
; PRIOR FILING DATE: 2001-10-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-280-576-3

Alignment Scores:
Pred. No.: 0.000117 Length: 3768
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 13 Gaps: 1

SEQ3-SEQ4 (1-30) x US-10-280-576-3 (1-3768)
Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuGluAspMetGlyAsp 27
Db 2989 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCTGCTGGAGGACGATGACATGGGGGAC 3048

Qy 28 LeuValAsp 30
Db 3049 CTGGTGGAT 3057

RESULT 16
US-09-765-973-1
; Sequence 1, Application US/09765973
; Publication No. US20020039573A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Hand-Zimmermann, Susan
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR PREVENTION AND
; TITLE OF INVENTION: TREATMENT OF HER-2/neu ASSOCIATED MALIGNANCIES
; FILE REFERENCE: 210121.496
; CURRENT APPLICATION NUMBER: US/09/765,973
; CURRENT FILING DATE: 2001-01-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-09-765-973-1

Alignment Scores:
Pred. No.: 0.000117 Length: 3768
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 13 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-765-973-1 (1-3768)
```

Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 2989 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3048
Qy 28 LeuValAsp 30
Db 3049 CTGGTGGAT 3057

RESULT 17
US-10-313-644-1
; Sequence 1, Application US/10313644
; Publication No. US20030157119A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: Hand-Zimmerman, Susan
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL
; TITLE OF INVENTION: AND VIRUS-ASSOCIATED MALIGNANCIES
; FILE REFERENCE: 210121.483C3
; CURRENT APPLICATION NUMBER: US/10/313,644
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-10-313-644-1

Alignment Scores: Length: 3768
Pred. No.: 0.000117 Matches: 20
Score: 89.00 Conservative: 0
Percent Similarity: 86.96% Mismatches: 1
Best Local Similarity: 86.96% Indels: 2
Query Match: 56.33% Gaps: 1
DB:

SEQ3-SEQ4 (1-30) x US-10-313-644-1 (1-3768)

Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 2989 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3048
Qy 28 LeuValAsp 30
Db 3049 CTGGTGGAT 3057

RESULT 18
US-09-441-411-5
; Sequence 5, Application US/09441411
; Publication No. US2003008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-441-411-5

Alignment Scores: Length: 4473
Pred. No.: 0.000144

Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 10 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-441-411-5 (1-4473)

Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 3163 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3222
Qy 28 LeuValAsp 30
Db 3223 CTGGTGGAT 3231

RESULT 19
US-10-146-473-32
; Sequence 32, Application US/10146473
; Publication No. US20030108888A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146,473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-473-32

Alignment Scores: Length: 4473
Pred. No.: 0.000144 Matches: 20
Score: 89.00 Conservative: 0
Percent Similarity: 86.96% Mismatches: 1
Best Local Similarity: 86.96% Indels: 2
Query Match: 56.33% Gaps: 1
DB: 15

SEQ3-SEQ4 (1-30) x US-10-146-473-32 (1-4473)

Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 3163 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3222
Qy 28 LeuValAsp 30
Db 3223 CTGGTGGAT 3231

RESULT 20
US-10-207-655-44
; Sequence 44, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44

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; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-207-655-44

Alignment Scores:
Pred. No.: 0.000144 Length: 4473
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 15 Gaps: 1

SEQ3-SEQ4 (1-30) x US-10-207-655-44 (1-4473)
Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 3163 GCCAGTCCCTTGGACAGCAGCCTTCTACCGCTCTGCTGGAGGACGATGACATGGGGGAC 3222
Qy 28 LeuValAsp 30
Db 3223 CTGGTGGAT 3231

RESULT 21
US-10-101-510-81
; Sequence 81, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-81

Alignment Scores:
Pred. No.: 0.000144 Length: 4473
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 15 Gaps: 1

SEQ3-SEQ4 (1-30) x US-10-101-510-81 (1-4473)
Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 3163 GCCAGTCCCTTGGACAGCAGCCTTCTACCGCTCTGCTGGAGGACGATGACATGGGGGAC 3222
Qy 28 LeuValAsp 30
Db 3223 CTGGTGGAT 3231

RESULT 22
US-09-877-177-11
; Sequence 11, Application US/09877177
; Publication No. US20020192652A1
; GENERAL INFORMATION:
; APPLICANT: Peter V. Danenberg et al.
; TITLE OF INVENTION: Method of determining Epidermal Growth
; FILE REFERENCE: 11220/120
; CURRENT APPLICATION NUMBER: US/09/877,177
; CURRENT FILING DATE: 2001-06-11
```

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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-877-177-11

Alignment Scores:
Pred. No.: 0.000146 Length: 4530
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 9 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-877-177-11 (1-4530)
Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 3139 GCCAGTCCCTTGGACAGCAGCCTTCTACCGCTCTGCTGGAGGACGATGACATGGGGGAC 3198
Qy 28 LeuValAsp 30
Db 3199 CTGGTGGAT 3207

RESULT 23
US-10-392-113-45
; Sequence 45, Application US/10392113
; Publication No. US20030224993A1
; GENERAL INFORMATION:
; APPLICANT: Land, Hartmut
; TITLE OF INVENTION: COMPOSITIONS THAT INHIBIT PROLIFERATION
; FILE REFERENCE: 21108.0005U3
; CURRENT APPLICATION NUMBER: US/10/392,113
; PRIOR FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: 60/365,078
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: PCT/US01/32127
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/239,705
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Descriptive Construct
US-10-392-113-45

Alignment Scores:
Pred. No.: 0.000146 Length: 4530
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 13 Gaps: 1

SEQ3-SEQ4 (1-30) x US-10-392-113-45 (1-4530)
Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 3139 GCCAGTCCCTTGGACAGCAGCCTTCTACCGCTCTGCTGGAGGACGATGACATGGGGGAC 3198
Qy 28 LeuValAsp 30
Db 3199 CTGGTGGAT 3207
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RESULT 24
US-10-426-836-11
; Sequence 11, Application US/10426836
; Publication No. US20030211530A1
; GENERAL INFORMATION:
; APPLICANT: K. Danenberg
; TITLE OF INVENTION: Method of determining Epidermal Growth
; TITLE OF INVENTION: Factor Receptor and HER2-Neu Gene Expression
; TITLE OF INVENTION: and Correlation of Levels Thereof With Survival
; FILE REFERENCE: 11220/169
; CURRENT APPLICATION NUMBER: US/10/426,836
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-426-836-11

Alignment Scores:
Pred. No.: 0.000146 Length: 4530
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 13 Gaps: 1

SEQ3-SEQ4 (1-30) x US-10-426-836-11 (1-4530)
Qy 10 AlaserProLeu-----ThrSerTyArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 3139 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3198
Qy 28 LeuValAsp 30
Db 3199 CTGGTGGAT 3207

RESULT 25
US-10-177-293-125
; Sequence 125, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
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; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-177-293-125

Alignment Scores:
Pred. No.: 0.000146 Length: 4530
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 15 Gaps: 1

SEQ3-SEQ4 (1-30) x US-10-177-293-125 (1-4530)
Qy 10 AlaserProLeu-----ThrSerTyArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 3139 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3198
Qy 28 LeuValAsp 30
Db 3199 CTGGTGGAT 3207

RESULT 26
US-10-007-926A-119
; Sequence 119, Application US/10007926A
; Publication No. US20030143539A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: HOULGATTE, REMI
; APPLICANT: BIRNBAUM, DANIEL
; APPLICANT: NGUYEN, CATHERINE
; APPLICANT: VIENS, PATRICE
; APPLICANT: FERT, VINCENT
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007,926A
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 119
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: v-erb-b2 avian erythroblastic leukemia viral
; OTHER INFORMATION: oncogene homolog 2 (neuro/glioblastoma derived
; OTHER INFORMATION: oncogene homolog) (ERBB2) gene.
US-10-007-926A-119

Alignment Scores:
Pred. No.: 0.000146 Length: 4530
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 15 Gaps: 1

SEQ3-SEQ4 (1-30) x US-10-007-926A-119 (1-4530)
Qy 10 AlaserProLeu-----ThrSerTyArgSerLeuLeuGluAspAspMetGlyAsp 27
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-437A-27

Alignment Scores:
Pred. No.:      0.000146      Length:      4530
Score:          89.00      Matches:      20
Percent Similarity: 86.96%      Conservative: 0
Best Local Similarity: 86.96%      Mismatches: 1
Query Match:      56.33%      Indels:      2
DB:              16      Gaps:      1

SEQ3-SEQ4 (1-30) x US-10-272-437A-27 (1-4530)

Qy      10 AlaSerProLeu-----ThrSerTyrArgSerLeuGluAspAspMetGlyAsp 27
Db      3139 GCCAGTCCCTTGGACACACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3198

Qy      28 LeuValAsp 30
Db      3199 CTGGTGGAT 3207
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Search completed: June 8, 2004, 09:24:13
Job time : 284 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 8, 2004, 04:50:51 ; Search time 62 Seconds
(without alignments)
268.525 Million cell updates/sec

Title: SEQ3-SEQ5

Perfect score: 159

Sequence: 1 DKGCPAQRASPLTSQNDLGPASPLDSTP 30

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp
-Q/cgn2_1/USPTO_spool_p/HOLLERAN480/runat_07062004_152435_24765/app_query.fasta_1.398
-DB=Issued Patents NA -QMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human4.0.cdi
-LIST=100 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=30
-MODE=LOCAL -OUTFWT=pt0 -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	52.8	2385	2	US-09-146-283-3
2	84	52.8	2385	3	US-08-579-823A-3
3	84	52.8	2385	3	US-09-344-195-3
4	80	50.3	153	3	US-08-776-251-3
5	80	50.3	201	4	US-09-200-355-3
6	80	50.3	816	3	US-08-776-251-10
7	80	50.3	3768	2	US-08-625-101-1
8	80	50.3	3768	2	US-08-356-786-1
9	80	50.3	3768	4	US-09-811-115-2
10	80	50.3	4473	2	US-09-048-804-1
11	80	50.3	4473	3	US-09-056-105-26
12	80	50.3	4473	4	US-09-663-834A-3

13	80	50.3	4530	1	US-08-229-515A-9	Sequence 9, Appli
14	80	50.3	4530	1	US-08-645-865-9	Sequence 9, Appli
15	80	50.3	4530	4	US-09-167-322-4	Sequence 4, Appli
16	80	50.3	4530	4	US-09-527-487-1	Sequence 1, Appli
17	80	50.3	4530	4	US-09-877-177A-11	Sequence 11, Appli
18	80	50.3	9274	4	US-09-811-115-1	Sequence 1, Appli
19	74	46.5	3955	1	US-08-229-515A-14	Sequence 14, Appli
20	74	46.5	3955	1	US-08-645-865-14	Sequence 14, Appli
C 21	59	37.1	11282	4	US-09-754-250-3	Sequence 3, Appli
C 22	58.5	36.8	634	1	US-08-451-947-1	Sequence 1, Appli
C 23	58.5	36.8	634	2	US-08-424-826A-1	Sequence 1, Appli
C 24	58.5	36.8	634	3	US-08-928-694-1	Sequence 1, Appli
C 25	58.5	36.8	634	4	US-08-450-842-1	Sequence 1, Appli
C 26	58.5	36.8	634	4	US-08-451-390-1	Sequence 1, Appli
C 27	58.5	36.8	634	5	PCT-US91-06950-1	Sequence 1, Appli
C 28	58.5	36.8	1404	1	US-07-796-106-22	Sequence 22, Appli
C 29	58.5	36.8	4403765	3	US-09-103-840A-2	Sequence 2, Appli
C 30	58.5	36.8	4411529	3	US-09-103-840A-1	Sequence 1, Appli
C 31	57	35.8	1938	4	US-09-547-435-25	Sequence 25, Appli
C 32	57	35.8	2316	4	US-09-547-435-27	Sequence 27, Appli
C 33	57	35.8	2604	4	US-09-547-435-23	Sequence 23, Appli
C 34	57	35.8	3384	4	US-09-547-435-29	Sequence 29, Appli
C 35	55.5	34.9	2691	4	US-09-020-743-1	Sequence 1, Appli
C 36	55	34.6	960	3	US-08-651-136C-1	Sequence 1, Appli
C 37	55	34.6	960	4	US-09-229-911A-1	Sequence 1, Appli
C 38	55	34.6	4092	3	US-09-306-595C-5	Sequence 5, Appli
C 39	55	34.6	4092	4	US-09-925-388-5	Sequence 5, Appli
C 40	55	34.6	5046	4	US-09-548-938A-5	Sequence 5, Appli
C 41	54.5	34.3	824	4	US-09-312-283C-369	Sequence 369, App
C 42	54	34.0	883	4	US-09-833-381-210	Sequence 210, App
C 43	53.5	33.6	685	1	US-08-451-947-7	Sequence 7, Appli
C 44	53.5	33.6	685	2	US-08-424-826A-7	Sequence 7, Appli
C 45	53.5	33.6	685	3	US-08-928-694-7	Sequence 7, Appli
C 46	53.5	33.6	685	4	US-08-450-842-7	Sequence 7, Appli
C 47	53.5	33.6	685	4	US-08-451-390-7	Sequence 7, Appli
C 48	53.5	33.6	685	5	PCT-US91-06950-7	Sequence 9, Appli
C 49	53.5	33.6	1190	1	US-08-451-947-9	Sequence 9, Appli
C 50	53.5	33.6	1190	2	US-08-424-826A-9	Sequence 9, Appli
C 51	53.5	33.6	1190	3	US-08-928-694-9	Sequence 9, Appli
C 52	53.5	33.6	1190	4	US-08-450-842-9	Sequence 9, Appli
C 53	53.5	33.6	1190	4	US-08-451-390-9	Sequence 9, Appli
C 54	53.5	33.6	1190	5	PCT-US91-06950-9	Sequence 9, Appli
C 55	53.5	33.6	32998	4	US-09-408-020-1	Sequence 1, Appli
C 56	53	33.3	963	4	US-09-252-991A-6814	Sequence 6814, Ap
C 57	53	33.3	1081	2	US-08-708-856A-13	Sequence 13, Appli
C 58	53	33.3	1081	3	US-09-287-375-13	Sequence 13, Appli
C 59	53	33.3	1081	4	US-09-455-406-13	Sequence 13, Appli
C 60	53	33.3	1368	4	US-09-328-352-430	Sequence 430, App
C 61	53	33.3	7174	4	US-08-961-527-189	Sequence 189, App
C 62	53	33.3	12047	2	US-09-022-461-1	Sequence 1, Appli
C 63	53	33.3	12047	3	US-09-033-556-3	Sequence 3, Appli
C 64	53	33.3	12047	4	US-09-474-699-11	Sequence 11, Appli
C 65	53	33.3	12047	4	US-09-151-376-3	Sequence 3, Appli
C 66	52.5	33.0	5766	4	US-09-566-921-39	Sequence 39, Appli
C 67	52	32.7	392000	4	US-10-027-983-11	Sequence 11, Appli
C 68	51.5	32.4	34063	4	US-09-453-702B-96	Sequence 96, Appli
C 69	51	32.1	873	4	US-09-489-039A-1911	Sequence 1911, Ap
C 70	51	32.1	1434	1	US-09-023-655-481	Sequence 481, App
C 71	51	32.1	1845	1	US-07-732-962A-1	Sequence 1, Appli
C 72	51	32.1	1845	2	PCT-US92-06106-1	Sequence 1, Appli
C 73	51	32.1	2256	5	US-08-318-826A-5	Sequence 5, Appli
C 74	51	32.1	2256	2	US-08-370-156-1	Sequence 1, Appli
C 75	51	32.1	2256	3	US-08-814-095-1	Sequence 1, Appli
C 76	51	32.1	3016	2	US-08-318-826A-7	Sequence 7, Appli
C 77	51	32.1	3016	2	US-08-370-156-5	Sequence 5, Appli
C 78	51	32.1	3016	3	US-08-814-095-5	Sequence 5, Appli
C 79	51	32.1	3096	2	US-08-318-826A-6	Sequence 6, Appli
C 80	51	32.1	3096	2	US-08-370-156-3	Sequence 3, Appli
C 81	51	32.1	3096	3	US-08-814-095-3	Sequence 3, Appli
C 82	51	32.1	3911	4	US-09-566-921-61	Sequence 61, Appli
C 83	51	32.1	7672	4	US-09-220-132-24	Sequence 24, Appli
C 84	51	32.1	8310	3	US-08-870-126-11	Sequence 11, Appli
C 85	51	32.1	8310	4	US-09-445-247-11	Sequence 11, Appli

Db 1976 GCACCGCGCTGCGCCAGCCAGCACA 2005

RESULT 3

US-09-344-195-3
; Sequence 3, Application US/09344195
; Patent No. 6210662
; GENERAL INFORMATION:
; APPLICANT: Laus, Reiner
; Ruegg, Curtis L.
; Wu, Hongyu
; TITLE OF INVENTION: Immunostimulatory Compositions
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave. Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/344,195
; FILING DATE: 24-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,283
; FILING DATE: 03-SEPT-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Judge, Linda R.
; REGISTRATION NUMBER: 42,702
; REFERENCE/DOCKET NUMBER: 7636-0010.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2385 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig. 8
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-344-195-3

Alignment Scores:
Pred. No.: 0.00569 Length: 2385
Score: 84.00 Matches: 21
Percent Similarity: 70.00% Conservative: 0
Best Local Similarity: 70.00% Mismatches: 5
Query Match: 52.83% Indels: 4
DB: 3 Gaps: 2

SEQ3-SEQ5 (1-30) x US-09-344-195-3 (1-2385)

Qy 1 AsplyGlyCysProAlaGluGlnArgAlaSerProLeuThrSergInAenGluAspLeu 20
Db 1925 GACAAGGCGCTGCGCCGAGCAGAGCCCTCTGAGTCCCTCGAG----- 1975

Qy 21 GlyProAla---SerProLeuAspSerThr 29

Db 1976 GCACCGCGCTGCGCCAGCCAGCACA 2005

RESULT 4

US-08-776-251-3
; Sequence 3, Application US/08776251
; Patent No. 6025340
; GENERAL INFORMATION:
; APPLICANT: Springer, Caroline J
; APPLICANT: Marais, Richard
; TITLE OF INVENTION: Surface expression of enzyme in gene directed prodrug therapy
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye
; STREET: 1100 No. 6025340th Glebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,251
; FILING DATE: 31-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01782
; FILING DATE: 27-JUL-1995
; APPLICATION NUMBER: GB 9415167.7
; FILING DATE: 27-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Arthur R. Crawford
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 620-20
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 153 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-776-251-3

Alignment Scores:
Pred. No.: 0.000697 Length: 153
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 3 Gaps: 0

SEQ3-SEQ5 (1-30) x US-08-776-251-3 (1-153)

Qy 1 AsplyGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
Db 10 GACAAGGCGCTGCGCCGAGCAGAGCCCTCTGAGCTCC 54

RESULT 5

US-09-200-355-3
; Sequence 3, Application US/09200355
; Patent No. 6451524
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; TITLE OF INVENTION: Identification Of Disease Predictive Nucleic Acids
; FILE REFERENCE: IBIS0009
; CURRENT APPLICATION NUMBER: US/09/200,355
; CURRENT FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 201
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-200-355-3

Alignment Scores:
Pred. No.: 0.000983 Length: 201
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 4 Gaps: 0

SEQ3-SEQ5 (1-30) x US-09-200-355-3 (1-201)

QY 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
DB 116 GACAGGGCGGCGCCCGCAGCAGAGCCGCCUUCGACGUCC 160

RESULT 6
US-08-776-251-10
; Sequence 10, Application US/08776251
; Patent No. 6025340
; GENERAL INFORMATION:
; APPLICANT: Springer, Caroline J
; APPLICANT: Marais, Richard
; TITLE OF INVENTION: Surface expression of enzyme in gene directed prodrug therapy
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye
; STREET: 1100 No. 6025340th Glebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 31-JAN-1997
; PRIOR APPLICATION NUMBER: US/08/776,251
; APPLICATION NUMBER: PCT/GB95/01782
; FILING DATE: 27-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9415167.7
; FILING DATE: 27-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Arthur R. Crawford
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 620-20
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 816 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-776-251-10

Alignment Scores:
Pred. No.: 0.00576 Length: 816
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 3 Gaps: 0

SEQ3-SEQ5 (1-30) x US-08-776-251-10 (1-816)

QY 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
DB 93 GACAGGGCGGCGCCCGCAGCAGAGCCGCCUUCGACGUCC 137

RESULT 7
US-08-625-101-1
; Sequence 1, Application US/08625101

Patent No. 5869445
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
; TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
; TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
; TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/625,101
; FILING DATE: 01-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3768 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3765
US-08-625-101-1

Alignment Scores:
Pred. No.: 0.0397 Length: 3768
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 2 Gaps: 0

SEQ3-SEQ5 (1-30) x US-08-625-101-1 (1-3768)

QY 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
DB 1915 GACAGGGCGGCGCCCGCAGCAGAGCCGCCUUCGACGUCC 1959

RESULT 8
US-08-356-786-1
; Sequence 1, Application US/08356786
; Patent No. 5877305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; TITLE OF INVENTION: Marker
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
; STREET: Exchange Place, 53 State Street
; CITY: Boston

APPLICANT: WU, YUNQI
TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
CORRESPONDENCE ADDRESS:
FILE REFERENCE: 233/221
CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER FILING DATE: 1997-04-10
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 26
LENGTH: 4473
TYPE: DNA
ORGANISM: Homo sapiens
US-09-056-105-26

Alignment Scores:
Pred. No.: 0.0494 Length: 4473
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 3 Gaps: 0

SEQ3-SEQ5 (1-30) x US-09-056-105-26 (1-4473)

Qy 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
Db 2089 GACAAGGGCTGCCCCCGAGCAGAGAGCCGCTCTGACGTC 2133

RESULT 12
US-09-663-834A-3
Sequence 3, Application US/09663834A
Patent No. 6613567
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF HER-2 EXPRESSION
FILE REFERENCE: RTS-0033
CURRENT APPLICATION NUMBER: US/09/663,834A
CURRENT FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 48
SEQ ID NO 3
LENGTH: 4473
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (175)...(3942)
US-09-663-834A-3

Alignment Scores:
Pred. No.: 0.0494 Length: 4473
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 4 Gaps: 0

SEQ3-SEQ5 (1-30) x US-09-663-834A-3 (1-4473)

Qy 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
Db 2089 GACAAGGGCTGCCCCCGAGCAGAGAGCCGCTCTGACGTC 2133

RESULT 13
US-08-229-515A-9
Sequence 9, Application US/08229515A
Patent No. 5518885
GENERAL INFORMATION:
APPLICANT: RAZIUDIN
APPLICANT: SARKAR, FAZLUL H
TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN

TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
STATE: Georgia
COUNTRY: usa
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,515A
FILING DATE: 19 APR 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.608
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
TELEFAX: 404-688-9880
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4530 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-229-515A-9

Alignment Scores:
Pred. No.: 0.0501 Length: 4530
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 1 Gaps: 0

SEQ3-SEQ5 (1-30) x US-08-229-515A-9 (1-4530)

Qy 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
Db 2065 GACAAGGGCTGCCCCCGAGCAGAGAGCCGCTCTGACGTC 2109

RESULT 14
US-08-645-865-9
Sequence 9, Application US/08645865
Patent No. 5654406
GENERAL INFORMATION:
APPLICANT: RAZIUDIN
APPLICANT: SARKAR, FAZLUL H
TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
STATE: Georgia
COUNTRY: usa
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,865
FILING DATE: 14 MAY 1996
CLASSIFICATION: 435

```

; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414,608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4530 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-645-865-9

Alignment Scores:
Pred. No.: 0.0501 Length: 4530
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 1 Gaps: 0

SEQ3-SEQ5 (1-30) x US-08-645-865-9 (1-4530)

Qy 1 AsplvsglyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
Db 2065 GACAAAGGCTGCCCGCCGAGCAGAGCCAGCCCTCTGACGTC 2109

RESULT 15
US-09-167-322-4
; Sequence 4, Application US/09167322
; Patent No. 6365151
; GENERAL INFORMATION:
; APPLICANT: Allegheny University of the Health
; Sciences, Halpern, Michael S.
; England, James W.
; TITLE OF INVENTION: CANCER VACCINE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorigna & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/167,322
; FILING DATE: 07-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/00582
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 7933-33 PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4530 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-167-322-4

```

```

Alignment Scores:
Pred. No.: 0.0501 Length: 4530
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 4 Gaps: 0

SEQ3-SEQ5 (1-30) x US-09-167-322-4 (1-4530)

Qy 1 AsplvsglyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
Db 2065 GACAAAGGCTGCCCGCCGAGCAGAGCCAGCCCTCTGACGTC 2109

RESULT 16
US-09-527-487-1
; Sequence 1, Application US/09527487
; Patent No. 6528060
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: HER2 ANTIGENIC PEPTIDES
; FILE REFERENCE: 126881309200
; CURRENT APPLICATION NUMBER: US/09/527,487
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (151)..(3915)
US-09-527-487-1

Alignment Scores:
Pred. No.: 0.0501 Length: 4530
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 4 Gaps: 0

SEQ3-SEQ5 (1-30) x US-09-527-487-1 (1-4530)

Qy 1 AsplvsglyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
Db 2065 GACAAAGGCTGCCCGCCGAGCAGAGCCAGCCCTCTGACGTC 2109

RESULT 17
US-09-877-177A-11
; Sequence 11, Application US/09877177A
; Patent No. 6582919
; GENERAL INFORMATION:
; APPLICANT: K. Danenberg
; TITLE OF INVENTION: Method of determining Epidermal Growth
; Factor Receptor and HER2-Neu Gene Expression
; TITLE OF INVENTION: and Correlation of Levels Thereof With Survival
; FILE REFERENCE: 11220/120
; CURRENT APPLICATION NUMBER: US/09/877,177A
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-877-177A-11

Alignment Scores:
Pred. No.: 0.0501 Length: 4530
Score: 80.00 Matches: 15

```

```
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 50.31%              Indels: 0
DB: 4                            Gaps: 0

SEQ3-SEQ5 (1-30) x US-09-877-177A-11 (1-4530)

QY 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
DB 2065 GACAAGGGTGTCCCGCCGAGCAGAGAGCCCTCTGACGTCC 2109

RESULT 18
US-09-811-115-1
; Sequence 1, Application US/09811115
; Patent No. 6632979
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GEMT.034A
; CURRENT APPLICATION NUMBER: US/09/811,115
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9274
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Vector Sequence
US-09-811-115-1

Alignment Scores:
Pred. No.: 0.124      Length: 9274
Score: 80.00          Matches: 15
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 50.31%              Indels: 0
DB: 4                  Gaps: 0

SEQ3-SEQ5 (1-30) x US-09-811-115-1 (1-9274)

QY 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
DB 3645 GACAAGGGTGTCCCGCCGAGCAGAGAGCCCTCTGACGTCC 3689

RESULT 19
US-08-229-515A-14
; Sequence 14, Application US/08229515A
; Patent No. 551885
; GENERAL INFORMATION:
; APPLICANT: RAZIYUDDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,865
; FILING DATE: 14 MAY 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3955 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-645-865-14
; Alignment Scores:
Pred. No.: 0.328      Length: 3955
Score: 74.00          Matches: 13
Percent Similarity: 100.00%      Conservative: 2
Best Local Similarity: 86.67%     Mismatches: 0
Query Match: 46.54%             Indels: 0
DB: 1                  Gaps: 0
```

```
SEQ3-SEQ5 (1-30) x US-08-229-515A-14 (1-3955)

QY 16 GlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe 30
DB 2999 CAGAACGAGGACTTGGGCCCATCCAGCCCATGGACAGTACCTTC 3043

RESULT 20
US-08-645-865-14
; Sequence 14, Application US/08645865
; Patent No. 5654406
; GENERAL INFORMATION:
; APPLICANT: RAZIYUDDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,865
; FILING DATE: 14 MAY 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3955 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-645-865-14
; Alignment Scores:
Pred. No.: 0.328      Length: 3955
Score: 74.00          Matches: 13
Percent Similarity: 100.00%      Conservative: 2
Best Local Similarity: 86.67%     Mismatches: 0
Query Match: 46.54%             Indels: 0
DB: 1                  Gaps: 0
```

Pred. No.: 0.328 Length: 3955
 Score: 74.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 2
 Best Local Similarity: 86.67% Mismatches: 0
 Query Match: 46.54% Indels: 0
 DB: 1 Gaps: 0

SEQ3-SEQ5 (1-30) x US-08-645-865-14 (1-3955)
 Qy 16 GlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe 30
 Db 2999 CAGACGAGGACTTGGGCCCATCCAGGCCCATGACAGTACCTTC 3043

RESULT 21
 US-09-754-250-3/c
 ; Sequence 3, Application US/09754250
 ; Patent No. 6376225
 ; GENERAL INFORMATION:
 ; APPLICANT: WEI, Ming-Hui et al
 ; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
 ; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
 ; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
 ; FILE REFERENCE: CL001063
 ; CURRENT APPLICATION NUMBER: US/09/754, 250
 ; CURRENT FILING DATE: 2001-01-05
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 111282
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(111282)
 ; OTHER INFORMATION: n = A, T, C or G
 US-09-754-250-3

Alignment Scores:
 Pred. No.: 3.71e+03 Length: 111282
 Score: 59.00 Matches: 11
 Percent Similarity: 56.52% Conservative: 2
 Best Local Similarity: 47.83% Mismatches: 10
 Query Match: 37.11% Indels: 0
 DB: 4 Gaps: 0

SEQ3-SEQ5 (1-30) x US-09-754-250-3 (1-111282)
 Qy 3 GlyCysProAlaGluGlnArgAlaSerProLeuThrSerGlnAsnGluAspLeuGlyPro 22
 Db 15912 GGCTGTCCAGCCCTGCTCATGCTCCCTCATGAGGAGGAGCTCATCCCTGCTCTCCC 15853

Qy 23 AlaSerPro 25
 Db 15852 ACCGAGCCC 15844

RESULT 22
 US-08-451-947-1/c
 ; Sequence 1, Application US/08451947
 ; Patent No. 5702906
 ; GENERAL INFORMATION:
 ; APPLICANT: GENENTECH, INC.
 ; APPLICANT: ROSENTHAL, ARNON
 ; TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
 ; NUMBER OF SEQUENCES: 100
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: patin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/451,947
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/426419
 ; FILING DATE: 19-APR-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/030013
 ; FILING DATE: 22-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/648482
 ; FILING DATE: 31-JAN
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/587707
 ; FILING DATE: 1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Torchia, Timothy B.
 ; REGISTRATION NUMBER: 36,700
 ; REFERENCE/DOCKET NUMBER: 666P2C1D2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-8674
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 634 bases
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-451-947-1

Alignment Scores:
 Pred. No.: 6.47 Length: 634
 Score: 58.50 Matches: 13
 Percent Similarity: 64.29% Conservative: 5
 Best Local Similarity: 46.43% Mismatches: 9
 Query Match: 36.79% Indels: 1
 DB: 1 Gaps: 1

SEQ3-SEQ5 (1-30) x US-08-451-947-1 (1-634)
 Qy 3 GlyCysProAlaGluGlnArgAlaSerProLeuThrSerGlnAsnGluAspLeuGlyPro 22
 Db 221 GGGGCACTGCTGACTCCCGAAGGCCCTCCAGCAGGAGCAGGAGGGGGCCCA 162
 Qy 23 Ala---SerProLeuAspSerThr 29
 Db 161 GCAGGGGCACCCCTAGACAGGACT 138

RESULT 23
 US-08-424-826A-1/c
 ; Sequence 1, Application US/08424826A
 ; Patent No. 5830858
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosenthal, Arnon
 ; TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
 ; NUMBER OF SEQUENCES: 98
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,826A
; FILING DATE: 19-APR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/240387
; FILING DATE: 10-May-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/648482
; FILING DATE: 31-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/587707
; FILING DATE: 25-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P06666P1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8674
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 634 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-424-826A-1

Alignment Scores:
Pred. No.: 6.47 Length: 634
Score: 58.50 Matches: 13
Percent Similarity: 64.29% Conservative: 5
Best Local Similarity: 46.43% Mismatches: 9
Query Match: 36.73% Indels: 1
DB: 2 Gaps: 1

SEQ3-SEQ5 (1-30) x US-08-424-826A-1 (1-634)

QY 3 GlyCysProAlaGluGlnArgAlaSerProLeuThrSerGlnAsnGluAspLeuGlyPro 22
DB 221 GGGGCACTGCTGACTCCGGAAGGCCCGAGCTCCAGCAGGAGAGCAGAGGGGGCCCA 162
QY 23 Ala---SerProLeuAspSerThr 29
DB 161 GCAGGGGCACTCCCTAGCAGGACT 138

RESULT 24

US-08-928-694-1/c
; Sequence 1, Application US/08928694
; Patent No. 6037320
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, ARNON
; TITLE OF INVENTION: NOVEL NEUTROTROPIC FACTOR
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,694
; FILING DATE: 12-Sep-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/451947

FILING DATE: 26-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/426419
; FILING DATE: 19-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/030013
; FILING DATE: 22-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/648482
; FILING DATE: 31-JAN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/587707
; FILING DATE: 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P06666P2C1D2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 634 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-928-694-1

Alignment Scores:
Pred. No.: 6.47 Length: 634
Score: 58.50 Matches: 13
Percent Similarity: 64.29% Conservative: 5
Best Local Similarity: 46.43% Mismatches: 9
Query Match: 36.73% Indels: 1
DB: 3 Gaps: 1

SEQ3-SEQ5 (1-30) x US-08-928-694-1 (1-634)

QY 3 GlyCysProAlaGluGlnArgAlaSerProLeuThrSerGlnAsnGluAspLeuGlyPro 22
DB 221 GGGGCACTGCTGACTCCGGAAGGCCCGAGCTCCAGCAGGAGAGCAGAGGGGGCCCA 162
QY 23 Ala---SerProLeuAspSerThr 29
DB 161 GCAGGGGCACTCCCTAGCAGGACT 138

RESULT 25

US-08-450-842-1/c
; Sequence 1, Application US/08450842
; Patent No. 6506728
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: ROSENTHAL, ARNON
; TITLE OF INVENTION: NOVEL NEUTROTROPIC FACTOR
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,842
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/426419


```

; REFERENCE/DOCKET NUMBER: 666P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/266-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 634 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US91-06950-1

Alignment Scores:
Pred. No.: 6.47 Length: 634
Score: 58.50 Matches: 13
Percent Similarity: 64.29% Conservative: 5
Best Local Similarity: 46.43% Mismatches: 9
Query Match: 36.79% Indels: 1
DB: 5 Gaps: 1

SEQ3-SEQ5 (1-30) x PCT-US91-06950-1 (1-634)
QY 3 GlyCysProAlaGluGlnArgAlaSerProLeuThrSerGlnAsnGluAspLeuGlyPro 22
Db 221 GGGGCACTGCTGACTCCCGAAAGGCCCGCCAGCTCCAGCAGGAAGAGCAGAGGGGGCCCA 162
QY 23 Ala---SerProLeuAspSerThr 29
Db 161 GCAGGGGCAACCCCTAGACAGGACT 138

RESULT 28
US-07-796-106-22/c
; Sequence 22, Application US/07796106
; Patent No. 5389529
; GENERAL INFORMATION:
; APPLICANT: PANAYOTATOS, NIKOS
; APPLICANT: FANDL, JAMES P.
; TITLE OF INVENTION: Production and Recovery of Recombinant
; TITLE OF INVENTION: Neurotrophins
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07796,106
; FILING DATE: 19911121
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6526-081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:

; REFERENCE/KEY: CDS
; LOCATION: 460...1104
; US-07-796-106-22

Alignment Scores:
Pred. No.: 17.7 Length: 1404
Score: 58.50 Matches: 13
Percent Similarity: 64.29% Conservative: 5
Best Local Similarity: 46.43% Mismatches: 9
Query Match: 36.79% Indels: 1
DB: 1 Gaps: 1

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Db 695 GGGGCACTGCTGACTCCCGAAAGGCCCGCCAGCTCCAGCAGGAAGAGCAGAGGGGGCCCA 636
QY 23 Ala---SerProLeuAspSerThr 29
Db 635 GCAGGGGCAACCCCTAGACAGGACT 612

RESULT 29
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
; US-09-103-840A-2

Alignment Scores:
Pred. No.: 3.88e+05 Length: 4403765
Score: 58.50 Matches: 12
Percent Similarity: 62.50% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 8
Query Match: 36.79% Indels: 1
DB: 3 Gaps: 1

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QY 22 ProAlaSerPro 25
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RESULT 30
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.

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; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

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Alignment Scores:
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Query Match:      36.79%      Indels:       1
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SEQ3-SEQ5 (1-30) x US-09-103-840A-1 (1-4411529)

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Qy      22 ProAlaSerPro 25
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Db 2327231 CCGCACCCACCC 2327242

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Search completed: June 8, 2004, 09:35:20
Job time : 2202 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 8, 2004, 06:43:09 ; Search time 267 Seconds
(without alignments)
512.584 Million cell updates/sec

Title: SEQ3-SEQ5
Perfect score: 159
Sequence: 1 DKGCPAQRASPLTSQNEGLGPASPLDSTF 30

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2995936 seqs, 2280998010 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Database : Published Applications NA:

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- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq*
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- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	80	50.3	884	16	US-10-412-804A-7	Sequence 7, Appli
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4	80	50.3	2164	16	US-10-412-804A-5	Sequence 5, Appli
5	80	50.3	3765	15	US-10-207-498-5	Sequence 5, Appli
6	80	50.3	3768	9	US-09-811-123-8	Sequence 8, Appli
7	80	50.3	3768	9	US-09-811-115-2	Sequence 2, Appli
8	80	50.3	3768	9	US-09-854-356-9	Sequence 9, Appli
9	80	50.3	3768	9	US-09-930-125-1	Sequence 1, Appli
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21	80	50.3	4530	15	US-10-177-293-125	Sequence 125, Appli
22	80	50.3	4530	15	US-10-007-926A-119	Sequence 119, Appli
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36	79	49.7	1115	15	US-10-102-806-165	Sequence 165, Appli
37	79	49.7	1713	15	US-10-378-393-14	Sequence 14, Appli
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39	79	49.7	1767	9	US-09-930-125-4	Sequence 4, Appli
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60	59	37.1	111282	14	US-10-094-989-3	Sequence 12, Appli
61	58.5	36.8	633	8	US-09-788-188-12	Sequence 1, Appli
62	58.5	36.8	634	13	US-08-450-842-1	Sequence 1, Appli
63	58.5	36.8	634	13	US-10-371-003-1	Sequence 13, Appli
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68	57	35.8	1938	15	US-10-422-264-25	Sequence 27, Appli
69	57	35.8	2316	15	US-10-422-264-27	Sequence 23, Appli
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73 57 35.8 3384 15 US-10-422-264-39
74 57 35.8 96898 16 US-10-417-476-33
75 56 35.2 401 9 US-09-960-352-9802
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78 56 35.2 1156 9 US-09-925-300-360
79 55.5 34.9 2691 9 US-09-967-768A-292
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83 55 34.6 368 9 US-09-880-107-1928
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ALIGNMENTS

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US-10-109-213-3
; Sequence 3, Application US/10109213
; Publication No. US20020168670A1
; GENERAL INFORMATION:
; APPLICANT: Eckert, David J.
; TITLE OF INVENTION: Identification Of Disease Predictive Nucleic Acids
; FILE REFERENCE: IBIS0009
; CURRENT APPLICATION NUMBER: US/10/109,213
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US/09/200,355
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 201
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-109-213-3
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Alignment Scores:
Pred. No.: 0.00095 Length: 201
Score: 80.00 Matches: 15
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
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QY 1 AspLysGlyCyProAlaGluGlnArgAlaSerProLeuThrSer 15
Db 116 GACAAAGGGCTGCGCCCGCAGCAGAGAGCCGCCUUCAGCGTCC 160
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RESULT 2
US-10-412-804A-7
; Sequence 7, Application US/10412804A
; Publication No. US20030228606A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuguan
; APPLICANT: Tatarewicz, Suzanna
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; TITLE OF INVENTION: HER-2 Receptor Tyrosine Kinase Molecules and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 01-1624-A
; CURRENT APPLICATION NUMBER: US/10/412,804A
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,912
; PRIOR FILING DATE: 2002-04-11
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 884
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (77)..(568)
US-10-412-804A-7

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Query Match: 50.31% Indels: 0
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; Publication No. US20030228606A1
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; APPLICANT: Jing, Shuguan
; APPLICANT: Tatarewicz, Suzanna
; TITLE OF INVENTION: HER-2 Receptor Tyrosine Kinase Molecules and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 01-1624-A
; CURRENT APPLICATION NUMBER: US/10/412,804A
; CURRENT FILING DATE: 2003-04-11
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; PRIOR FILING DATE: 2002-04-11
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; NAME/KEY: unsure
; LOCATION: (1169)
; OTHER INFORMATION: "n" can be a, g, c, or t
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US-10-412-804A-1
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Query Match: 50.31% Indels: 0
DB: 16 Gaps: 0

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; APPLICANT: Jirg, Shuqian
; APPLICANT: Tatarewicz, Suzanna
; TITLE OF INVENTION: HER-2 Receptor Tyrosine Kinase Molecules and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 01-1624-A
; CURRENT APPLICATION NUMBER: US/10/412,804A
; CURRENT FILING DATE: 2003-04-11
; PRIOR FILING DATE: 2003-04-11
; PRIOR FILING DATE: 60/371,912
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2164
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2160)
US-10-412-804A-5
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Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
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RESULT 5
US-10-207-498-5
; Sequence 5, Application US/10207498
; Publication No. US20030143568A1
; GENERAL INFORMATION:
; APPLICANT: Elizabeth Singer
; APPLICANT: Ralf Landgraf
; APPLICANT: Dennis J. Slamon
; APPLICANT: David Eisenberg
; TITLE OF INVENTION: METHODS AND MATERIALS FOR CHARACTERIZING
; TITLE OF INVENTION: AND MODULATING INTERACTIONS BETWEEN HERGULIN AND HER3
; FILE REFERENCE: 30448.103-US-U1
; CURRENT APPLICATION NUMBER: US/10/207,498
; CURRENT FILING DATE: 2002-07-29
; PRIOR FILING DATE: 60/308,431
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
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Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
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US-09-811-123-8
; Sequence 8, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
; APPLICANT: Ralph Schwall
; APPLICANT: Mark Slikowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ERBB
; TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
; FILE REFERENCE: GENENT.073A2
; CURRENT APPLICATION NUMBER: US/09/811,123
; CURRENT FILING DATE: 2001-03-16
; PRIOR FILING DATE: 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-123-8
Alignment Scores:
Pred. No.: 0.0232 Length: 3768
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
Gaps: 0
DB: 9

SEQ3-SEQ5 (1-30) x US-09-811-123-8 (1-3768)
Qy 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
|||||
Db 1915 GACAAAGGGCTGCCCCCGGAGAGAGAGCCAGCCCTCTGACGTCC 1959
|||||
RESULT 7
US-09-811-115-2
; Sequence 2, Application US/09811115
; Patent No. US20020035736A1
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT.034A
; CURRENT APPLICATION NUMBER: US/09/811,115
; CURRENT FILING DATE: 2001-03-16
; PRIOR FILING DATE: 60/189,844
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-115-2
Alignment Scores:
Pred. No.: 0.0232 Length: 3768
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
```

Score: 80.00 Matches: 15
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.31% Indels: 0
 DB: 9 Gaps: 0

SEQ3-SEQ5 (1-30) x US-09-811-115-2 (1-3768)

QY 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 |||||
 Db 1915 GACAGGGCTGCCCCCGCAGAGAGCCGCTCTGACGTC 1959

RESULT 8

US-09-854-356-9
 ; Sequence 9, Application US/09854356
 ; Patent No. US2002017567A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: Gheysen, Dirk
 ; APPLICANT: Corixa Corporation
 ; APPLICANT: SmithKline Beecham Biologicals S. A.
 ; TITLE OF INVENTION: HER-2/neu Fusion Proteins
 ; FILE REFERENCE: 014058-009810PC
 ; CURRENT APPLICATION NUMBER: US/09/854,356
 ; CURRENT FILING DATE: 2001-05-09
 ; PRIOR APPLICATION NUMBER: US 09/493,480
 ; PRIOR FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: US 60/117,976
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 9
 ; LENGTH: 3768
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(3768)
 ; OTHER INFORMATION: human HER-2/neu protein
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(1959)
 ; OTHER INFORMATION: extracellular domain (ECD) of human HER-2/neu
 ; NAME/KEY: misc feature
 ; LOCATION: (2026)..(3765)
 ; OTHER INFORMATION: intracellular domain (ICD) of human HER-2/neu
 ; NAME/KEY: misc feature
 ; LOCATION: (2968)..(3765)
 ; OTHER INFORMATION: phosphorylation domain (PD) of human HER-2/neu
 ; NAME/KEY: misc feature
 ; LOCATION: (2968)..(3144)
 ; OTHER INFORMATION: preferred portion of the phosphorylation domain
 ; OTHER INFORMATION: (delta PD) of human HER-2/neu
 US-09-854-356-9

Alignment Scores:
 Pred. No.: 0.0232 Length: 3768
 Score: 80.00 Matches: 15
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.31% Indels: 0
 DB: 9 Gaps: 0

SEQ3-SEQ5 (1-30) x US-09-854-356-9 (1-3768)

QY 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 |||||
 Db 1915 GACAGGGCTGCCCCCGCAGAGAGCCGCTCTGACGTC 1959

RESULT 9

US-09-930-125-1
 ; Sequence 1, Application US/09930125
 ; Publication No. US20020193329A1
 ; GENERAL INFORMATION:

; APPLICANT: Hand-Zimmerman, Susan
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: Foy, Teresa M.
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Vedvick, Thomas S.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS
 ; FILE REFERENCE: 210121.544
 ; CURRENT APPLICATION NUMBER: US/09/930,125
 ; CURRENT FILING DATE: 2001-08-14

; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FastSeq For Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 3768
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(3765)
 US-09-930-125-1

Alignment Scores:
 Pred. No.: 0.0232 Length: 3768
 Score: 80.00 Matches: 15
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.31% Indels: 0
 DB: 9 Gaps: 0

SEQ3-SEQ5 (1-30) x US-09-930-125-1 (1-3768)

QY 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 |||||
 Db 1915 GACAGGGCTGCCCCCGCAGAGAGCCGCTCTGACGTC 1959

RESULT 10

US-09-984-092-3
 ; Sequence 3, Application US/09984092
 ; Publication No. US20040037840A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pharmexa A/S
 ; TITLE OF INVENTION: NOVEL THERAPEUTIC VACCINE FORMULATIONS
 ; FILE REFERENCE: P1011PC00
 ; CURRENT APPLICATION NUMBER: US/09/984,092
 ; CURRENT FILING DATE: 2001-10-26
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 3768
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(3768)
 US-09-984-092-3

Alignment Scores:
 Pred. No.: 0.0232 Length: 3768
 Score: 80.00 Matches: 15
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.31% Indels: 0
 DB: 13 Gaps: 0

SEQ3-SEQ5 (1-30) x US-09-984-092-3 (1-3768)

QY 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 |||||
 Db 1915 GACAGGGCTGCCCCCGCAGAGAGCCGCTCTGACGTC 1959

RESULT 11

US-10-280-576-3
 ; Sequence 3, Application US/10280576
 ; Publication No. US2004004405A1
 ; GENERAL INFORMATION:

; APPLICANT: Wolff, Matthew R.
 ; TITLE OF INVENTION: VASCULAR STENT OR GRAFT COATED OR IMPREGNATED WITH PROTEIN
 ; FILE REFERENCE: 09820.189
 ; CURRENT APPLICATION NUMBER: US/10/280,576
 ; CURRENT FILING DATE: 2002-10-22
 ; PRIOR APPLICATION NUMBER: 60/343,732
 ; PRIOR FILING DATE: 2001-10-25
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3
 ; LENGTH: 3768
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-280-576-3

Alignment Scores:
 Pred. No.: 0.0232 Length: 3768
 Score: 80.00 Matches: 15
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.31% Indels: 0
 DB: 13 Gaps: 0

SEQ3-SEQ5 (1-30) x US-10-280-576-3 (1-3768)

Qy 1 AsplyGlyCysProAlaGluInArgAlaSerProLeuThrSer 15
 |||||
 Db 1915 GACAAGGGCTGCCCGCCGAGAGAGAGCCAGCCCTCTGACGTCC 1959

RESULT 12

US-09-765-973-1
 ; Sequence 1, Application US/09765973
 ; Publication No. US20020039573A1
 ; GENERAL INFORMATION:

; APPLICANT: Cheever, Martin A.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR PREVENTION AND
 ; TITLE OF INVENTION: TREATMENT OF HER-2/neu ASSOCIATED MALIGNANCIES
 ; FILE REFERENCE: 210121.496
 ; CURRENT APPLICATION NUMBER: US/09/765,973
 ; CURRENT FILING DATE: 2001-01-19

; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 3768
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(3765)
 US-09-765-973-1

Alignment Scores:
 Pred. No.: 0.0232 Length: 3768
 Score: 80.00 Matches: 15
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.31% Indels: 0
 DB: 13 Gaps: 0

SEQ3-SEQ5 (1-30) x US-09-765-973-1 (1-3768)

Qy 1 AsplyGlyCysProAlaGluInArgAlaSerProLeuThrSer 15
 |||||
 Db 1915 GACAAGGGCTGCCCGCCGAGAGAGAGCCAGCCCTCTGACGTCC 1959

RESULT 13

US-10-313-644-1
 ; Sequence 1, Application US/10313644

; Publication No. US20030157119A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: Hand-Zimmerman, Susan
 ; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL
 ; TITLE OF INVENTION: AND VIRUS-ASSOCIATED MALIGNANCIES
 ; FILE REFERENCE: 210121.483C3
 ; CURRENT APPLICATION NUMBER: US/10/313,644
 ; CURRENT FILING DATE: 2002-12-04
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 3768
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(3765)
 US-10-313-644-1

Alignment Scores:
 Pred. No.: 0.0232 Length: 3768
 Score: 80.00 Matches: 15
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.31% Indels: 0
 DB: 15 Gaps: 0

SEQ3-SEQ5 (1-30) x US-10-313-644-1 (1-3768)

Qy 1 AsplyGlyCysProAlaGluInArgAlaSerProLeuThrSer 15
 |||||
 Db 1915 GACAAGGGCTGCCCGCCGAGAGAGAGCCAGCCCTCTGACGTCC 1959

RESULT 14

US-09-441-411-5
 ; Sequence 5, Application US/09441411
 ; Publication No. US2003008342A1
 ; GENERAL INFORMATION:

; APPLICANT: Scholler, Nathalie B.
 ; APPLICANT: Disig, Mary L.
 ; APPLICANT: Hellstrom, Ingegerd
 ; APPLICANT: Hellstrom, Karl Erik
 ; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
 ; FILE REFERENCE: 730033.409
 ; CURRENT APPLICATION NUMBER: US/09/441,411
 ; CURRENT FILING DATE: 1999-11-16

; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 4473
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-441-411-5

Alignment Scores:
 Pred. No.: 0.0279 Length: 4473
 Score: 80.00 Matches: 15
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.31% Indels: 0
 DB: 10 Gaps: 0

SEQ3-SEQ5 (1-30) x US-09-441-411-5 (1-4473)

Qy 1 AsplyGlyCysProAlaGluInArgAlaSerProLeuThrSer 15
 |||||
 Db 2089 GACAAGGGCTGCCCGCCGAGAGAGAGCCAGCCCTCTGACGTCC 2133

RESULT 15

US-10-146-473-32
 ; Sequence 32, Application US/10146473

Publication No. US2003010888A1
 GENERAL INFORMATION:
 APPLICANT: Scanlan, Matthew
 APPLICANT: Gout, Ivan
 APPLICANT: Stockert, Elisabeth
 APPLICANT: Gure, Ali
 APPLICANT: Chen, Yao-Tsang
 APPLICANT: Old, Lloyd
 TITLE OF INVENTION: Breast Cancer Antigens
 FILE REFERENCE: L00461/70130(JRV)
 CURRENT APPLICATION NUMBER: US/10/146,473
 CURRENT FILING DATE: 2002-05-15
 PRIOR APPLICATION NUMBER: US 60/291,150
 PRIOR FILING DATE: 2001-05-15
 NUMBER OF SEQ ID NOS: 82
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 32
 LENGTH: 4473
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-146-473-32

Alignment Scores:
 Pred. No.: 0.0279 Length: 4473
 Score: 80.00 Matches: 15
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.31% Indels: 0
 DB: 15 Gaps: 0

SEQ3-SEQ5 (1-30) x US-10-146-473-32 (1-4473)

QY 1 AsPLySGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 |||||
 DB 2089 GACAGGGCTGCCCGCCGAGCAGAGAGCCCTCTGACGTCC 2133

RESULT 16

US-10-207-655-44
 Sequence 44, Application US/10207655
 Publication No. US20030118592A1
 GENERAL INFORMATION:
 APPLICANT: Ledbetter, Jeffrey A.
 APPLICANT: Hayden-Ledbetter, Martha S.
 TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
 FILE REFERENCE: 390069.401C1
 CURRENT APPLICATION NUMBER: US/10/207,655
 CURRENT FILING DATE: 2002-07-25
 NUMBER OF SEQ ID NOS: 426
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 44
 LENGTH: 4473
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-207-655-44

Alignment Scores:
 Pred. No.: 0.0279 Length: 4473
 Score: 80.00 Matches: 15
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.31% Indels: 0
 DB: 15 Gaps: 0

SEQ3-SEQ5 (1-30) x US-10-207-655-44 (1-4473)

QY 1 AsPLySGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 |||||
 DB 2089 GACAGGGCTGCCCGCCGAGCAGAGAGCCCTCTGACGTCC 2133

RESULT 17

US-10-101-510-81
 Sequence 81, Application US/10101510
 Publication No. US20030148295A1

GENERAL INFORMATION:
 APPLICANT: WAN, JACKSON
 APPLICANT: WANG, YIXIN
 TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
 FILE REFERENCE: 15117.0012
 CURRENT APPLICATION NUMBER: US/10/101,510
 CURRENT FILING DATE: 2002-03-20
 PRIOR APPLICATION NUMBER: 60/276,947
 PRIOR FILING DATE: 2001-03-20
 NUMBER OF SEQ ID NOS: 805
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 81
 LENGTH: 4473
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-101-510-81

Alignment Scores:
 Pred. No.: 0.0279 Length: 4473
 Score: 80.00 Matches: 15
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.31% Indels: 0
 DB: 15 Gaps: 0

SEQ3-SEQ5 (1-30) x US-10-101-510-81 (1-4473)

QY 1 AsPLySGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 |||||
 DB 2089 GACAGGGCTGCCCGCCGAGCAGAGAGCCCTCTGACGTCC 2133

RESULT 18

US-09-877-177-11
 Sequence 11, Application US/09877177
 Publication No. US20020192652A1
 GENERAL INFORMATION:
 APPLICANT: Peter V. Danenberg et al.
 TITLE OF INVENTION: Method of determining Epidermal Growth
 Factor Receptor and HER2-New Gene Expression
 FILE REFERENCE: 11220/120
 CURRENT APPLICATION NUMBER: US/09/877,177
 CURRENT FILING DATE: 2001-06-11
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 11
 LENGTH: 4530
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-877-177-11

Alignment Scores:
 Pred. No.: 0.0283 Length: 4530
 Score: 80.00 Matches: 15
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.31% Indels: 0
 DB: 9 Gaps: 0

SEQ3-SEQ5 (1-30) x US-09-877-177-11 (1-4530)

QY 1 AsPLySGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 |||||
 DB 2065 GACAGGGCTGCCCGCCGAGCAGAGAGCCCTCTGACGTCC 2109

RESULT 19

US-10-392-113-45
 Sequence 45, Application US/10392113
 Publication No. US20030224993A1
 GENERAL INFORMATION:
 APPLICANT: Land, Hartmut
 APPLICANT: Deleu, Laurent
 TITLE OF INVENTION: COMPOSITIONS THAT INHIBIT PROLIFERATION
 OF CANCER CELLS

```

; FILE REFERENCE: 21108_0005U3
; CURRENT APPLICATION NUMBER: US/10/392,113
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: 60/365,078
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: PCT/US01/32127
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/239,705
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
US-10-392-113-45

Alignment Scores:
Pred. No.: 0.0283 Length: 4530
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 13 Gaps: 0

SEQ3-SEQ5 (1-30) x US-10-392-113-45 (1-4530)

Qy 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
|||||
Db 2065 GACAAGGGCTGCCCGCCGAGCAGAGCCAGCCCTCTGAGCTCC 2109

RESULT 20
US-10-426-836-11
; Sequence 11, Application US/10426836
; Publication No. US20030211530A1
; GENERAL INFORMATION:
; APPLICANT: K. Danenberg
; TITLE OF INVENTION: Method of determining Epidermal Growth
; TITLE OF INVENTION: Factor Receptor and HER2-Neu Gene Expression
; TITLE OF INVENTION: and Correlation of Levels Thereof With Survival
; FILE REFERENCE: 11220/169
; CURRENT APPLICATION NUMBER: US/10/426,836
; CURRENT FILING DATE: 2003-05-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-426-836-11

Alignment Scores:
Pred. No.: 0.0283 Length: 4530
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 13 Gaps: 0

SEQ3-SEQ5 (1-30) x US-10-426-836-11 (1-4530)

Qy 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
|||||
Db 2065 GACAAGGGCTGCCCGCCGAGCAGAGCCAGCCCTCTGAGCTCC 2109

RESULT 21
US-10-177-293-125
; Sequence 125, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Puzstai, Lajos
; APPLICANT: Mexic, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-177-293-125

Alignment Scores:
Pred. No.: 0.0283 Length: 4530
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 15 Gaps: 0

SEQ3-SEQ5 (1-30) x US-10-177-293-125 (1-4530)

Qy 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
|||||
Db 2065 GACAAGGGCTGCCCGCCGAGCAGAGCCAGCCCTCTGAGCTCC 2109

RESULT 22
US-10-007-926A-119
; Sequence 119, Application US/10007926A
; Publication No. US20030143539A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: HOULGATTE, REMI
; APPLICANT: BIRNBAUM, DANIEL
; APPLICANT: NGUYEN, CATHERINE
; APPLICANT: VIENS, PATRICE
; APPLICANT: FERT, VINCENT
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007,926A
; CURRENT FILING DATE: 2001-12-07

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RESULT 28
US-10-159-563-208
; Sequence 208, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meitner, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 208
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-159-563-208

Alignment Scores:
Pred. No.: 0.0283 Length: 4530
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 16 Gaps: 0

SEQ3-SEQ5 (1-30) x US-10-159-563-208 (1-4530)

Qy 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
|||||
Db 2065 GACAGGGCTGCCCCCGCGAGCAGAGAGCCAGCCCTCTGACGTC 2109

RESULT 29
US-10-435-696-10
; Sequence 10, Application US/10435696
; Publication No. US20040018525A1
; GENERAL INFORMATION:
; APPLICANT: Wirtz, Ralph
; APPLICANT: Munnes, Marc
; APPLICANT: Kallabis, Harald
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSIS, PR
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA
; FILE REFERENCE: Lea 36 108
; CURRENT APPLICATION NUMBER: US/10/435,696
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: EP03003112.4
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: EP02010291.9
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 314
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-435-696-10

Alignment Scores:
Pred. No.: 0.0283 Length: 4530
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 16 Gaps: 0

SEQ3-SEQ5 (1-30) x US-10-435-696-10 (1-4530)

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Qy 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
Db 2065 GACAAGGGCTGCCCCCGCGAGAGAGAGCCGCTCTGACGTCC 2109

RESULT 30

US-09-769-508-1
; Sequence 1, Application US/09769508
; Patent No. US20020155527A1
; GENERAL INFORMATION:
; APPLICANT: STUART, SUSAN G.
; APPLICANT: MONAHAN, JOHN J.
; APPLICANT: LANGTON, BEATRICE CLAUDIA
; APPLICANT: HANCOCK, MIRIAM E.C.
; APPLICANT: CHAO, LORRINE A.
; APPLICANT: BLUFORD, PETER
; TITLE OF INVENTION: C-ERBB-2 EXTERNAL DOMAIN: GP75
; FILE REFERENCE: BBIO-111-C1
; CURRENT APPLICATION NUMBER: US/09/769,508
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4543
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (150)..(3914)
US-09-769-508-1

Alignment Scores:
Pred. No.: 0.0284 Length: 4543
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 9 Gaps: 0

SEQ3-SEQ5 (1-30) x US-09-769-508-1 (1-4543)

Qy 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
Db 2064 GACAAGGGCTGCCCCCGCGAGAGAGAGCCGCTCTGACGTCC 2108

Search completed: June 8, 2004, 09:24:28
Job time : 282 secs